

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:21 : Search time 35.3333 Seconds

(without alignments)
37.723 Million cell updates/sec

Title: US-09-657-431-5

Perfect score: 75

Sequence: 1 RNPDDGVGCPWK 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	12	22	AAB92091
2	75	100.0	12	22	AAB36566
3	70	93.3	11	18	AAW34297
4	70	93.3	11	21	AAW34297
5	70	93.3	18	22	AAW34297
6	70	93.3	23	22	AAW34297
7	70	93.3	23	22	AAW34297
8	70	93.3	23	22	AAW34297
9	70	93.3	24	22	AAW34297
10	70	93.3	24	22	AAW34297
11	70	93.3	24	22	AAW34297

12	70	93.3	79	18	AAW19256
13	70	93.3	90	21	AAW1914
14	70	93.3	91	21	AAW58868
15	70	93.3	93	21	AAW1917
16	70	93.3	95	21	AAW1913
17	70	93.3	98	21	AAW1916
18	70	93.3	101	18	AAW34286
19	70	93.3	101	18	AAW34288
20	70	93.3	101	21	AAW1890
21	70	93.3	101	21	AAW1892
22	70	93.3	101	21	AAW1912
23	70	93.3	104	21	AAW1915
24	70	93.3	189	21	AAW1918
25	70	93.3	192	21	AAW1919
26	70	93.3	266	22	AAW32126
27	70	93.3	266	22	AAW32129
28	70	93.3	266	22	AAW32136
29	70	93.3	271	21	AAW18407
30	70	93.3	30	20	AAW25408
31	70	93.3	371	13	AAW22502
32	70	93.3	380	13	AAW22504
33	70	93.3	437	19	AAW51457
34	70	93.3	453	20	AAW95051
35	70	93.3	467	13	AAW22499
36	70	93.3	476	13	AAW22503
37	70	93.3	566	20	AAW02100
38	70	93.3	790	15	AAW60519
39	70	93.3	790	22	AAW36562
40	70	93.3	791	18	AAW34285
41	70	93.3	791	21	AAW1887
42	70	93.3	791	21	AAW9589
43	70	93.3	791	21	AAW50867
44	70	93.3	791	22	AAW67223
45	70	93.3	807	13	AAW20013

ALIGNMENTS

RESULT 1
AAB92091
ID AAB92091 standard; Peptide; 12 AA.
AC AAB92091:
XX 22-JUN-2001 (first entry)
DE Laminin fragment SEQ ID NO:1267.
XX
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200069900-A2.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US13576.
XX
XX 17-MAY-1999; 99US-0134406.
XX 10-SEP-1999; 99US-0153406.
XX 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX
PS Disclosure; Page 610; 733pp; English.
XX
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (II) and a
CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidease stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
CC
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 75; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RNPdGVGGPWK 12
Db 1 RNPdGVGGPWK 12
RESULT 2
AAB36566
ID AAB36566 standard; Peptide; 12 AA.
AC AAB36566;
XX
DT 09-MAR-2001 (first entry)
XX
DE Mammalian kringle 5 peptide SEQ ID NO:5.
XX
KW Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory;
KW vasotrophic; cytosolic; antirheumatic; antipruritic; antidiabetic;
KW antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogenesis;
KW inflammatory disorder; inflammation; chronic articular rheumatism;
KW psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis;
KW capillary proliferation; atherosclerotic plaque; osteoporosis;
KW cancer; solid tumour; angiodioma; retrolental fibroplasia;
KW haemangioma; Kasposi's sarcoma; neovascularisation; tumour growth.
XX
XX
OS Mammalia.
XX
PN WO200070665-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-IB00763.
XX
PR 17-MAY-1999; 99US-0134406.
XX
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Rasamoeliso M, Thibaudau K, Huang X, Belliveau R;
XX
XX WPI; 2001-090970/10.
XX
XX New modified anti-angiogenic kringle 5 peptides capable of forming
PT conjugates with blood proteins, useful for treating angiogenesis,
PT inappropriate invasion of vessels or cancers in humans or mammals
XX

PS Claim 5; Page 9; 82pp; English.
XX
XX
CC The present invention describes a modified anti-angiogenic peptide (I)
CC comprising a reactive group that reacts with amino groups, hydroxyl
CC groups or thiol groups on blood components to form stable covalent
CC bonds. The reactive group is selected from succinimide or maleimido
CC groups. (I) can have anti-inflammatory, vasotropic, cytosolic,
CC antirheumatic, antipruritic, antidiabetic, antarteriosclerotic and
CC osteopathic activities, and is an angiogenesis inhibitor. (I) are useful
CC for treating angiogenesis in a human, where the derivative is reacted
CC with blood proteins. (I) are also useful for manufacturing a medicament
CC extending the in vivo half-life of a kringle 5 peptide in a patient to
CC provide an anti-angiogenic effect. In particular, a modified kringle 5
CC peptide can be used for treating inflammatory disorders (e.g. immune and
CC non-immune inflammation, chronic articular rheumatism or psoriasis),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis,
CC capillary proliferation in atherosclerotic plaques or osteoporosis), or
CC cancer associated disorders (e.g. solid tumours, solid tumour
CC metastases, angiodiomas, retrolental fibroplasia, haemangiomas,
CC Kasposi's sarcoma or other cancers requiring neovascularisation to
CC support tumour growth). The peptides are useful for treating these
CC diseases in mammalian or human patients. AAB36562 represents a mammalian
CC kringle 5 protein, and AAB36563 to AAB36577 represent specifically
CC claimed kringle 5 peptides from the present invention.
CC
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 75; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RNPdGVGGPWK 12
Db 1 RNPdGVGGPWK 12
RESULT 3
AAW34297
ID AAW34297 standard; peptide; 11 AA.
AC AAW34297;
XX
DT 14-MAY-1998 (first entry)
XX
DE Kringle 5 peptide fragment.
XX
KW Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
KW metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
KW psoriasis; arthritis; macular degeneration; diabetic retinopathy;
KW autoimmune disease; ocular disease; capillary proliferation; therapy;
KW kringle 5 receptor.
XX
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note="N-Ac-Arg"
FT Modified-site 11 /note="C-terminal amide"
XX
XX
PN WO9741824-A2.
XX
PD 13-NOV-1997.
XX
PF 05-MAY-1997; 97WO-US07700.
XX
XX 03-APR-1997; 97US-0832087.
XX 03-MAY-1996; 96US-0643219.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Davidson DJ, Gubbins EJ, Wang J;

PA (NOON) UNIV NORTHWESTERN.
 XX
 PI Soff G, Gately ST, Twardowski P;
 XX
 DR WPI: 2001-550019/61.
 XX
 PT Producing angiotensin for treating angiogenic diseases involves
 PT contacting plasminogen with plasminogen activator and sulfhydryl donor
 PT simultaneously, or producing plasmin which is contacted with sulfhydryl
 PT donor
 XX
 PS Example 7; Page 47; 101pp; English.
 XX
 CC The specification describes a method for generating angiotensin in
 CC vitro. The method comprises contacting plasminogen with a sulfhydryl
 CC donor, or culturing cells capable of producing plasminogen activator
 CC in conditioned culture medium (CCM) and contacting the CCM with
 CC plasminogen. Angiotensin produced by method of the invention is useful
 CC for treating animals with angiogenesis diseases. It is useful for
 CC treating an angiogenic disease such as neoplastic diseases (e.g. tumours
 CC and tumour metastasis), benign tumours (e.g. hemangiomas, acoustic
 CC neuromas, etc), connective tissue disorders (e.g. rheumatoid arthritis
 CC and atherosclerosis), ocular angiogenic diseases (e.g. diabetic
 CC retinopathy, corneal graft rejection, etc), cardiovascular diseases,
 CC cerebral vascular diseases, diabetes-associated diseases and immune
 CC disorders (e.g. chronic inflammation and autoimmunity). The present
 CC sequence represents an antigenic peptide derived from human angiotensin.
 XX
 SQ Sequence 18 AA:
 XX
 Query Match 93.3%; Score 70; DB 22; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RNPdGVGGPW 11
 DB 1 RNPdGVGGPW 11
 XX
 RESULT 6
 AAB83293
 ID AAB83293 standard; peptide; 23 AA.
 XX
 AC AAB83293;
 XX
 DT 13-JUL-2001 (first entry)
 XX
 DE Kringie peptide #2.
 XX
 KW Pulmonary delivery; bioconjugation; pulmonary fluid protein; opioid;
 KW systemic drug delivery; antihistamine; anti-angina; anti-hypertensive;
 KW anti-arrhythmic; anti-depressant; bronchodilator; anti-inflammatory;
 KW anti-thyroid deficiency; Kringie.
 XX
 OS Synthetic.
 XX
 PN WO200117568-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2000WO-IB01429.
 XX
 PR 07-SEP-1999; 99US-0152681.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Erin AM, Fleser A, Robitaille M, Milner PG, Bridon DP;
 XX
 DR WPI: 2001-354657/37.
 XX
 PT Pulmonary delivery of therapeutic agents which are capable of forming
 PT covalent bonds with amino, hydroxyl or thiol groups on pulmonary or
 PT blood components

XX
 PS Example 13; Page 137; 184pp; English.
 XX
 CC The present invention describes a modified therapeutic agent comprising a
 CC therapeutic agent and a reactive group which reacts with groups on
 CC pulmonary or blood components to form a stable covalent bond, where the
 CC therapeutic agent may be a peptide. Pulmonary drug delivery is useful as
 CC it increases the drug retention-time in the lungs and reduces the risk of
 CC extrapulmonary side effects. Modified therapeutic agents of this type may
 CC be antihistamines, anti-angina, anti-hypertensive or anti-arrhythmic
 CC agents, anti-depressants, bronchodilators, opioids or their analogues,
 CC anti-inflammatory agents, or anti-thyroid deficiency agents. The present
 CC sequence is a kringie peptide.
 XX
 SQ Sequence 23 AA:
 XX
 Query Match 93.3%; Score 70; DB 22; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.0059;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RNPdGVGGPW 11
 DB 1 RNPdGVGGPW 11
 XX
 RESULT 7
 AAB92096
 ID AAB92096 standard; Peptide; 23 AA.
 XX
 AC AAB92096;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Laminin fragment SEQ ID NO:1272.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 XX
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US13576.
 XX
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Erin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI: 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 PS Disclosure; Page 611; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB50829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

CC Sequence 23 AA:

Query Match 93.3%; Score 70; DB 22; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNPDDGVGSPW 11
| | | | | | | | | | |
DB 1 RNPDDGVGSPW 11

RESULT 8
AAB36570
ID AAB36570 standard; Peptide: 23 AA.

AC AAB36570;

DT 09-MAR-2001 (first entry)

DE Mammalian kringle 5 peptide SEQ ID NO:9.

KW Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory;
KW vasotrophic; cytosolic; antineumatic; antiprotatic; antidiabetic;
KW antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogenesis;
KW inflammatory disorder; inflammation; chronic articular rheumatism;
KW psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis;
KW capillary proliferation; atherosclerotic plaque; osteoporosis;
KW cancer; solid tumour; angiofibroma; retrorenal fibroplasia;
KW haemangioma; Kaposi's sarcoma; neovascularisation; tumour growth.

OS Mammalia.

PN WO200070665-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-IB00763.

PR 17-MAY-1999; 99US-0134406.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Rasamolisolo M, Thibaudau K, Huang X, Beliveau R;

DR WPI: 2001-090970/10.

PT New modified anti-angiogenic kringle 5 peptides capable of forming
PT conjugates with blood proteins, useful for treating angiogenesis,
PT inappropriate invasion of vessels or cancers in humans or mammals

PS Claim 5; Page 9; 82pp; English.

CC The present invention describes a modified anti-angiogenic peptide (I)
CC comprising a reactive group that reacts with amino groups, hydroxyl
CC groups or thiol groups on blood components to form stable covalent
CC bonds. The reactive group is selected from succinimide or maleimido
CC groups. (I) can have anti-inflammatory, vasotrophic, cytosolic,
CC antineumatic, antiprotatic, antidiabetic, antiarteriosclerotic and
CC osteopathic activities, and is an angiogenesis inhibitor. (I) are useful
CC for treating angiogenesis in a human, where the derivative is reacted
CC with blood proteins. (I) are also useful for manufacturing a medicament
CC extending the in vivo half-life of a kringle 5 peptide in a patient to
CC provide an anti-angiogenic effect. In particular, a modified kringle 5
CC peptide can be used for treating inflammatory disorders (e.g. immune and

CC non-immune inflammation, chronic articular rheumatism or psoriasis),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis,
CC capillary proliferation in atherosclerotic plaques or osteoporosis), or
CC cancer associated disorders (e.g. solid tumours, solid tumour
CC metastases, angiofibromas, retrorenal fibroplasia, haemangiomas,
CC Kaposi's sarcoma or other cancers requiring neovascularisation to
CC support tumour growth). The peptides are useful for treating these
CC diseases in mammalian or human patients. AAB36562 represents a mammalian
CC kringle 5 protein, and AAB36563 to AAB36577 represent specifically
CC claimed kringle 5 peptides from the present invention.

CC Sequence 23 AA:

Query Match 93.3%; Score 70; DB 22; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNPDDGVGSPW 11
| | | | | | | | | | |
DB 1 RNPDDGVGSPW 11

RESULT 9
AAB92090
ID AAB92090 standard; Peptide: 24 AA.

AC AAB92090;

DT 22-JUN-2001 (first entry)

DE Laminin fragment SEQ ID NO:1266.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

KW Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI: 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure: Page 609; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases.
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 24 AA;

Query Match 93.3%; Score 70; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.0062;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNPBGDVGGPW 11
 |||||
 DB 1 RNPBGDVGGPW 11

RESULT 10

AAB92095
 ID AAB92095 standard; Peptide; 24 AA.

AC AAB92095;

DE 22-JUN-2001 (first entry)

Laminin fragment SEQ ID NO:1271.

Protection; endogenous therapeutic peptide; peptidase; conjugation;
 blood component; modification; succinimidy; maleimido group; amino;
 hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure: Page 611; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy) and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention.

XX SQ Sequence 24 AA;

Query Match 93.3%; Score 70; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.0062;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNPBGDVGGPW 11
 |||||
 DB 1 RNPBGDVGGPW 11

RESULT 11

AAB36565
 ID AAB36565 standard; Peptide; 24 AA.

AC AAB36565;

DE 09-MAR-2001 (first entry)

Mammalian kringle 5 peptide SEQ ID NO:4.

KW Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory;
 KW vasotropic; cytosolic; antirheumatic; antipruritic; antidiabetic;
 KW antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogenesis;
 KW inflammatory disorder; inflammation; chronic articular rheumatism;
 KW psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis;
 KW capillary proliferation; atherosclerotic plaque; osteoporosis;
 KW cancer; solid tumour; angiodioma; retrolental fibroplasia;
 KW haemangioma; Kasposi's sarcoma; neovascularisation; tumour growth.

OS Mammalia.

PN WO200070665-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-IB00763.

PR 17-MAY-1999; 99US-0134406.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Rasameolisolo M, Thibaudau K, Huang X, Beliveau R;

DR WPI; 2001-090970/10.

PT New modified anti-angiogenic kringle 5 peptides capable of forming
 PT conjugates with blood proteins, useful for treating angiogenesis,
 PT inappropriate invasion of vessels or cancers in humans or mammals
 XX Claim 5; Page 9; 82pp; English.

CC The present invention describes a modified anti-angiogenic peptide (I)
 CC comprising a reactive group that reacts with amino groups, hydroxyl
 CC groups or thiol groups on blood components to form stable covalent
 CC bonds. The reactive group is selected from succinimidy) or maleimido
 CC groups. (I) can have anti-inflammatory, vasotropic, cytosolic,
 CC antirheumatic, antipruritic, antidiabetic, antiarteriosclerotic and
 CC osteopathic activities, and is an angiogenesis inhibitor. (I) are useful
 CC for treating angiogenesis in a human, where the derivative is reacted
 CC with blood proteins. (I) are also useful for manufacturing a medicament
 CC extending the in vivo half-life of a kringle 5 peptide in a patient to
 CC provide an anti-angiogenic effect. In particular, a modified kringle 5
 CC peptide can be used for treating inflammatory disorders (e.g. immune and
 CC non-immune inflammation, chronic articular rheumatism or psoriasis),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis,
 CC capillary proliferation in atherosclerotic plaques or osteoporosis), or
 CC cancer associated disorders (e.g. solid tumours, solid tumour
 CC metastases, angiodiomas, retrolental fibroplasia, haemangiomas,
 CC Kasposi's sarcoma or other cancers requiring neovascularisation to

CC support tumour growth). The peptides are useful for treating these
 CC diseases in mammalian or human patients. AAB36562 represents a mammalian
 CC kringle 5 protein, and AAB36563 to AAB36577 represent specifically
 CC claimed kringle 5 peptides from the present invention.

XX Sequence 24 AA;

Query Match

93.3%; Score 70; DB 22; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.0062;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNPDDGVGGPW 11

DB 1 RNPDDGVGGPW 11

RESULT 12

AAM19256 AAM19256 standard; Peptide: 79 AA.

XX AAM19256;

DT 27-FEB-1998 (first entry)

DE Human plasminogen Kringle 5 fragment.

KW Plasminogen; Kringle 5; cell proliferation inhibitor; angiogenesis;
 diagnosis; therapeutic.

OS Homo sapiens.

PN WO9723500-A1.

PD 03-JUL-1997.

PF 13-DEC-1996; 96WO-US20447.

PR 12-DEC-1996; 96US-0763528.

PR 13-DEC-1995; 95US-0008519.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Cao Y, Folkman MJ;

DR WPI, 1997-350965/32.

PT Plasminogen Kringle 5 peptide - which inhibits endothelial cell
 PT proliferation, useful to treat angiogenesis mediated diseases and in
 PT detection and diagnosis

PS Claim 1; Page 8; 51pp; English.

CC This sequence is an isolated fragment of the Kringle 5 peptide
 CC corresponding to amino acid 462 of the human plasminogen protein which
 CC can be used in a novel method to inhibit endothelial cell proliferation
 CC activity. The protein can be used to treat angiogenesis mediated
 CC diseases, e.g. haemangioma, solid tumours, leukaemia, metastasis,
 CC telangiectasia, psoriasis, scleroderma, pyogenic granuloma, myocardial
 CC angiogenesis, plaque neovascularisation, coronary or cerebral
 CC collaterals, arteriovenous malformations, ischemic limb angiogenesis,
 CC corneal diseases, rubecosis, neovascular glaucoma, diabetic retinopathy,
 CC retrolental fibroplasia, arthritis, diabetic neovascularisation,
 CC muscular degeneration, peptic ulcer, Helicobacter related disease,
 CC fractures, keloids, vasculogenesis, haematopoiesis, ovulation,
 CC menstruation, placenta and cat scratch fever, and to stimulate wound
 CC healing. The protein and antibodies generated from it can be used to
 CC screen for agonists and antagonists or in detection, imaging and
 CC diagnosis.

XX Sequence 79 AA;

Query Match

93.3%; Score 70; DB 18; Length 79;

Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNPDDGVGGPW 11

DB 52 RNPDDGVGGPW 62

RESULT 13

AAB01914 AAB01914 standard; Protein: 90 AA.

XX AAB01914;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringle 5 (Val1454-Ala543).

KW Plasminogen; human; kringle domain; endothelial cell proliferation;
 KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
 KW antipsoriatic; antiinflammatory; antitumor; antirheumatic; antiarthritic;
 KW antiangiogenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

PN US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

PR 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

PA (ABBO) ABBOTT LAB.

PI Davidson DJ;

DR WPI, 2000-349573/30.

PT Preparation of Kringle five peptide fragment for treating various
 PT disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -

XX Example 17; Page -; 48pp; English.

CC The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
 CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukaemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Weber
 CC syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01906-B01919 represent fragments of human plasminogen used
 CC in an exemplification of the invention.
 CC Note: This sequence is not shown in the specification, but is derived
 CC from the full length human plasminogen sequence (AAB01887) shown in
 CC figure 1.

XX Sequence 90 AA;

Query Match

93.3%; Score 70; DB 21; Length 90;

Best Local Similarity 100.0%; Pred. No. 0.021;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:35:26 : Search time 16 seconds

(without alignments)
36.034 Million cell updates/sec

Title: US-09-657-431-11

Perfect score: 6

Sequence: 1 RKLXDY 6

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR-71:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	100.0	810	1	PLHM
2	6	100.0	812	1	PLMS
3	5	83.3	42	2	B42177
4	5	83.3	72	2	D82937
5	5	83.3	79	2	D97807
6	5	83.3	104	2	G81291
7	5	83.3	107	2	P86048
8	5	83.3	107	2	B91202
9	5	83.3	110	2	G70021
10	5	83.3	112	1	B29654
11	5	83.3	126	2	AE0091
12	5	83.3	129	2	S22688
13	5	83.3	177	2	S59643
14	5	83.3	181	1	A64477
15	5	83.3	187	2	T47984
16	5	83.3	190	2	B64358
17	5	83.3	205	2	B82601
18	5	83.3	209	2	A03894
19	5	83.3	215	2	A95406
20	5	83.3	231	2	T02765
21	5	83.3	232	2	A13304
22	5	83.3	234	2	A97652
23	5	83.3	234	2	AH2875
24	5	83.3	234	2	A84515
25	5	83.3	234	2	T52100
26	5	83.3	247	2	U00393
27	5	83.3	247	2	JC0532
28	5	83.3	248	2	AE0281
29	5	83.3	264	2	A71853

30	5	83.3	264	2	G97170
31	5	83.3	266	2	S59237
32	5	83.3	280	2	D71160
33	5	83.3	283	2	G75002
34	5	83.3	289	1	RLT7T
35	5	83.3	289	1	JC5606
36	5	83.3	305	2	E83852
37	5	83.3	307	2	A71602
38	5	83.3	322	2	A70661
39	5	83.3	326	2	D90241
40	5	83.3	336	2	D86710
41	5	83.3	368	2	F82570
42	5	83.3	376	2	A90206
43	5	83.3	376	2	E70361
44	5	83.3	379	2	S55900
45	5	83.3	379	2	T41633

ALIGNMENTS

RESULT 1
PLHM
Plasmin (EC 3.4.21.7) precursor [validated] - human
N:Alternate names: plasminogen precursor [misnomer]
C:Contains: angiotatin; microplasmin; plasminogen
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence-revision 02-Dec-1994 #text-change 15-Sep-2000
C:Accession: A35229; 152242; A26646; 162738; 184609; S03735; A00929; A04627; A04625;
R:Peterson, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A>Title: Characterization of the gene for human plasminogen, a key proenzyme in the
A:Reference number: A35229; M01D:90202679
A:Accession: A35229
A:Molecule type: DNA
A:Residues: 1-810 <PEP>
A:Cross-references: GB:J05286; GB:M34276; NID:9190064; PIDN:AAA60113.1; PID:9387026
A:Experimental source: leukocyte; lung fibroblast
R:Margaret, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.;
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A>Title: Definition of the transcription initiation site of human plasminogen gene in
A:Reference number: 152242; M01D:91097523
A:Accession: 152242
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <MAL3>
A:Cross-references: NID:M62890; NID:9190092; PIDN:AAA36454.1; PID:9553613
R:Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A>Title: Molecular cloning and characterization of a full-length cDNA clone for human
A:Reference number: A26646; M01D:87162490
A:Accession: A26646
A:Molecule type: mRNA
A:Residues: 1-471, 'D', 473-810 <FOR>
A:Cross-references: GB:X05199; NID:935530; PIDN:CAA28831.1; PID:935531
A:Experimental source: liver
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A>Title: Characterization of a complementary deoxyribonucleic acid coding for human a
A:Reference number: 145961; M01D:85023311
A:Accession: 162738
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 292-471, 'D', 473-810 <MAL2>
A:Cross-references: GB:X02922; NID:9190112; PIDN:AAA60124.1; PID:9387031
A:Accession: 184609
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 367-419 <MAL3>
A:Cross-references: GB:K02921; NID:9190110; PIDN:AAA60123.1; PID:9190111
R:Brundish, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg,
Eur. J. Biochem. 114, 465-470, 1981
A>Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma

- A:Reference number: S03735; MUID:81212097
A:Accession: S03735
A:Molecule type: protein
A:Residues: 20-71, 'E', 73-76 <BRD>
R:Storup-Jensen, L.; Petersen, T.E.; Magnusson, S.
Submitted to the Atlas, July 1977
A:Reference number: A00929
A:Accession: A00929
A:Molecule type: protein
A:Residues: 20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>
R:Wiman, B.
Eur. J. Biochem. 76, 129-137, 1977
A:Title: Primary structure of the B-chain of human plasmin.
A:Reference number: A04627; MUID:77225245
A:Accession: A04627
A:Molecule type: protein
A:Residues: 581-810 <WT1>
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen.
A:Reference number: A04625; MUID:75093329
A:Accession: A04625
A:Molecule type: protein
A:Residues: 20-50, 'Q', 51-71, 'E', 73-85, 87-100 <W12>
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen the A-chain.
A:Reference number: A04626; MUID:76043692
A:Accession: A04626
A:Molecule type: protein
A:Residues: 483-507, 'E', 509-604 <W13>
R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
J. Biol. Chem. 248, 1631-1633, 1973
A:Title: The primary structure of human plasminogen. II. The histidine loop of human plasminogen.
A:Reference number: A92125; MUID:73149248
A:Contents: annotation: active site
J.Groskopf, W.R.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of the A-chain.
A:Reference number: A92048; MUID:65234739
A:Contents: annotation: active site
R:Trexler, M.; Vall, Z.; Pathy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
A:Reference number: A92382; MUID:82213905
A:Contents: annotation: omega-aminocarboxylic acid binding sites
R:Vall, Z.; Pathy, L.
J. Biol. Chem. 259, 13690-13694, 1984
A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential for fibrin binding.
A:Reference number: A92458; MUID:85054794
A:Contents: annotation: fibrin binding site; omega-aminocarboxylic acid binding site
J.Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.
J. Biol. Chem. 271, 29461-29467, 1996
A:Title: Kringles domains of human angiotensin. Characterization of the anti-proliferative activity of the kringles.
A:Reference number: A58811; MUID:97067211
A:Contents: annotation
R:Lijnen, H.R.; Uguw, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A:Title: Generation of an angiotensin-like fragment from plasminogen by streptolysin-1 (M13).
A:Reference number: A58812; MUID:9548733
A:Contents: annotation
R:Tulinsky, A.; Mulichak, A.M.
Submitted to the Brookhaven Protein Data Bank, July 1991
A:Reference number: A51341; PDB:1PK4
A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
R:Tulinsky, A.; Wu, T.P.
Submitted to the Brookhaven Protein Data Bank, July 1991
A:Reference number: A51488; PDB:2PK4
A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
R:Wu, T.P.; Tulinsky, A.
Submitted to the Brookhaven Protein Data Bank, August 1993
A:Reference number: A51911; PDB:1PKR
A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
R:Padmanabhan, K.; Tulinsky, A.
Submitted to the Brookhaven Protein Data Bank, April 1994
A:Reference number: A52408; PDB:1PKM
A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
R:Tulinsky, A.; Mathews, I.I.
Submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A65244; PDB:1CEA
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R:Tulinsky, A.; Mathews, I.I.
Submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A65245; PDB:1CEB
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R:Mulichak, A.M.; Tulinsky, A.; Kavichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A:Title: Crystal and molecular structure of human plasminogen kringles 4 refined at 1.5 Å.
A:Reference number: A58819; MUID:92031502
A:Contents: annotation
R:Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A:Title: The refined structure of the epsilon-aminocaproic acid complex of human plasminogen.
A:Reference number: A58818; MUID:92031503
A:Contents: annotation
R:de Vos, A.M.; Utsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, J.D.
Biochemistry 31, 270-279, 1992
A:Title: Crystal structure of the kringles 2 domain of tissue plasminogen activator at 1.8 Å.
A:Reference number: A39483; MUID:92118803
A:Contents: annotation; X-ray crystallography, 2.4 angstroms
R:Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
Submitted to the Brookhaven Protein Data Bank, June 1995
A:Reference number: A65980; PDB:1KRN
A:Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
R:Rejzante, M.; Llinas, M.
Submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65803; PDB:1HPJ
A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A:Title: (1)H-NMR assignments and secondary structure of human plasminogen kringles 1 and 2.
A:Reference number: A36445; MUID:94237157
A:Contents: annotation; conformation by (1)H-NMR, residues 96-184
R:Rejzante, M.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen.
A:Reference number: A58817; MUID:94237158
A:Contents: annotation; conformation by (1)H-NMR
C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many tissues.
C:Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:OKH d PIR:GHBGB).
C:Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:IRHQA2) immediately after release from the fibrin-lysine complex.
C:Comment: Microplasmin is formed by autocatalytic cleavage of plasmin under artificial conditions.
C:Comment: Streptolysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiotensin.
C:Genetics:
A:Gene: GDB:PLG
A:Cross-references: GDB:119498; OMIM:173350
A:Map position: 6q26-6q27
A:Map position: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1;
C:Function:
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a number of tissues; also activates the urokinase-type plasminogen
A:Pathway: fibrinolysis
C:Superfamily: plasmin; kringles; plasminogen-related protein precursor homologs
C:Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; h
F1-96/Domain: plasminogen-related protein precursor homolog <PLPH>
F1-19/Domain: signal sequence <status predicted> <SIG>
F1-20-810/Product: plasminogen <status experimental> <PRO>
F1-20-96/Domain: activation peptide <status experimental> <APT>

F:79-466/Product: angiotatin #status experimental <AST>
F:97-580,581-810/Product: plasmin chain A #status experimental <MAT>
F:97-580/Domains: plasmin chain A #status experimental <CH>
F:103-181/Domains: kringle homology <KR1>
F:185-262/Domains: kringle homology <KR2>
F:275-352/Domains: kringle homology <KR3>
F:377-454/Domains: kringle homology <KR4>
F:481-560/Domains: kringle homology <KR5>
F:550-580,581-810/Product: micropasmin #status experimental <MMT>

Query Match 100.0%; Score 6; DB 1; Length 810;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLVD 6
Db 549 RKLVD 554

RESULT 2

PLMS
plasmin (EC 3.4.21.7) precursor - mouse
N:Contains: angiotatin; plasminogen
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
C:Accession: A38514; S48202; S48203
R:Degeen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics 8, 49-61, 1990

A:Title: Characterization of the CDNA coding for mouse plasminogen and localization of
A:Reference number: A38514; MUID:91184812
A:Accession: A38514

A:Molecule type: mRNA

A:Residues: 1-812 <DEG>

A:Cross-references: GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g200403

R:LiJnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.

Eur. J. Biochem. 224, 863-871, 1994

A:Title: Characterization of the murine plasma fibrinolytic system.

A:Reference number: S48202; MUID:95010076

A:Accession: S48202

A:Molecule type: protein

A:Residues: 20-25 <LID>

A:Accession: S48203

A:Molecule type: protein

A:Residues: 22-27 <LID>

C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many of
C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin
immediately after dissociation from the clot. In the presence of the inhibitor, the activa
e inhibitor, the activation involves also removal of the activation peptide.
C:Comment: Stromelysin 1 (see PIR:KCMS1) acts on plasminogen to produce angiotatin. Th
eul in treating solid tumors.

C:Function:
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
as the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A:Pathway: fibrinolysis

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: angiotatin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd

F:1-96/Domains: plasminogen-related protein precursor homology <PLPH>

F:1-19/Domains: signal sequence #status predicted <SIG>

F:20-812/Product: plasminogen #status predicted <PRO>

F:20-96/Domains: activation peptide #status predicted <APT>

F:79-466/Product: angiotatin #status predicted <AST>

F:97-581,582-812/Product: plasmin #status predicted <MAT>

F:97-581/Domains: chain A #status predicted <ACH>

F:103-181/Domains: kringle homology <KR1>

F:185-262/Domains: kringle homology <KR2>

F:275-352/Domains: kringle homology <KR3>

F:377-454/Domains: kringle homology <KR4>

F:481-560/Domains: kringle homology <KR5>

F:582-812/Domains: chain B #status predicted <BCH>

F:582-805/Domains: trypsin homology <TR>

F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32

bonds: #status predicted

F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted

F:136,308/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted
F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 100.0%; Score 6; DB 1; Length 812;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLVD 6
Db 549 RKLVD 554

RESULT 3

B42177
KRAB-domain-containing zinc finger protein D19S19 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000

C:Accession: B42177

R:Constantinou-Deltas, C.D.; Gilbert, J.; Bartlett, R.J.; Herbstreith, M.; Roses, A.D

Genomics 12, 581-589, 1992

A:Title: The identification and characterization of KRAB-domain-containing zinc finge

A:Reference number: A42177; MUID:92217982

A:Accession: B42177

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-42 <CON>

A:Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:95677, NCBI:95689)

C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 83.3%; Score 5; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLVD 5
Db 25 RKLVD 29

RESULT 4

D82937
conserved hypothetical U0080 [imported] - Ureaplasma urealyticum

C:Species: Ureaplasma urealyticum

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: D82937

R:Glass, J.I.; Leikowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.

submitted to GenBank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a

A:Reference number: A82870

A:Accession: D82937

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-72 <GAB>

A:Cross-references: GB:A002107; GB:AF222894; NID:g6699022; PIDN:AAF30485.1; GSPDB:GN

A:Experimental source: serovar 3; biovar 1

C:Genetics:

A:Gene: U0080

A:Genetic code: SGC3

Query Match 83.3%; Score 5; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLVD 5
Db 50 RKLVD 54

RESULT 5

D97607
ankyrin like protein [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
 C:Accession: D97807
 R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R
 Science 293, 2093-2098, 2001
 A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
 A:Reference number: A97700; MUID:21442074; PMID:11557893
 A:Accession: D97807
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-79 <R>
 A:Cross-references: GB:AE006914; PIDN:AAL03398.1; PID:g1561964; GSPDB:GN00173
 C:Genetics:
 A:Gene: RC0860

Query Match 83.3%; Score 5; DB 2; Length 79;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLVD 5
 |||||
 Db 21 RKLVD 25

RESULT 6
 G81291
 probable periplasmic protein Cj1456c [imported] - Campylobacter jejuni (strain NCTC 1116
 C:Species: Campylobacter jejuni
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 20-Apr-2000
 C:Accession: G81291
 R:Parhill, J.; Wren, B.W.; Mungall, K.; Kelley, J.M.; Churcher, C.; Basham, D.; Chilling
 C.W.; Quail, M.; Rajadream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
 Nature 403, 665-668, 2000
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf
 A:Reference number: A81230; MUID:20150912
 A:Accession: G81291
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-104 <PAR>
 A:Cross-references: GB:AL139078; GB:AL111168; NID:96966723; PIDN:CAB73879.1; PID:g696886
 A:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:
 A:Gene: Cj1456c
 C:Superfamily: Campylobacter jejuni probable periplasmic protein Cj1456c

Query Match 83.3%; Score 5; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KLYDY 6
 |||||
 Db 53 KLYDY 57

RESULT 7
 F86048
 hypothetical protein 25138 [imported] - Escherichia coli (strain O157:H7, substrain EDL5
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: F86048
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhek
 iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoustis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85460; MUID:21074935; PMID:11206351
 A:Accession: F86048
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-107 <STO>
 A:Cross-references: GB:AE005174; NID:g12518480; PIDN:AAG58850.1; GSPDB:GN00145; UMGF:251
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: 25138

Query Match 83.3%; Score 5; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLVD 5
 |||||
 Db 68 RKLVD 72

RESULT 8
 B91202
 hypothetical protein ECS4586 [imported] - Escherichia coli (strain O157:H7, substrain
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C:Accession: B91202
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
 A:Reference number: A9629; MUID:21156231; PMID:11258796
 A:Accession: B91202
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-107 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA838009.1; PID:g13364061; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RMD 0509952
 C:Genetics:
 A:Gene: ECS4586

Query Match 83.3%; Score 5; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLVD 5
 |||||
 Db 68 RKLVD 72

RESULT 9
 G70021
 hypothetical protein yusN - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
 C:Accession: G70021
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gal
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
 koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
 Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanl
 A:Authors: Schleich, S.; Schreier, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
 ekerchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiya
 T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumselto, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
 A:Reference number: A69580; MUID:98044033
 A:Accession: G70021
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-110 <RUN>
 A:Cross-references: GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CAB15275.1; PID:el1843
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yusN
 C:Superfamily: Bacillus subtilis hypothetical protein yusN

Query Match 83.3%; Score 5; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 37;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKLVD 5
 |||||
 Db 69 RKLVD 73

RESULT 10

B29654
 Proteinase inhibitor (PSTI type), submandibular - lion
 C:Species: Panthera leo (lion)
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
 C:Accession: B29654
 R:Reisinger, P.W.M.; Hochstrasser, K.; Goettlicher, I.; Eulitz, M.; Wachter, E.
 Biol.Chem. Hoppe-Seyler 368, 717-726, 1987
 A:Title: The amino-acid sequences of the double-headed proteinase inhibitors from cat,
 A:Reference number: A94650; PMID:87299011
 A:Accession: B29654
 A:Molecule type: protein
 A:Residues: 1-112 <REF>
 C:Superfamily: submandibular proteinase inhibitor; Kazal proteinase inhibitor homology
 C:Keywords: duplication; saliva; serine proteinase inhibitor; submandibular gland
 F:6-60/Domain: Kazal proteinase inhibitor homology <RP1>
 F:62-111/Domain: Kazal proteinase inhibitor homology <RP2>
 F:8-42,20-39,28-60,64-93,71-90,79-111/Disulfide bonds: #status predicted
 F:72/Inhibitory site: Lys (trypsin) #status predicted
 F:73/Inhibitory site: Met (chymotrypsin, elastase) #status predicted

Query Match 83.3%; Score 5; DB 1; Length 112;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVD 5
 |||||
 Db 53 RKLVD 57

RESULT 11

AE0091
 Probable flagellar protein flis [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AE0091
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibbells, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 H., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; PMID:21470413; PMID:11586360
 A:Accession: AE0091
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-126 <KUD>
 A:Cross-references: GB:AL590842; PIDN:CA089592.1; PID:915978824; GSPDB:GN00175
 C:Genetics:
 A:Gene: flis
 C:Superfamily: flagellar protein flis

Query Match 83.3%; Score 5; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKLVD 6
 |||||
 Db 86 RKLVD 90

RESULT 12

S22688
 LppA protein - Shigella flexneri virulence plasmid pWR100
 C:Species: Shigella flexneri
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
 C:Accession: S22688

R:Allaoui, A.; Mounier, J.; Prevost, M.C.; Sansonetti, P.J.; Parsot, C.
 Mol. Microbiol. 6, 1605-1616, 1992
 A:Title: icsB: a Shigella flexneri virulence gene necessary for the lysins of protrusi
 A:Reference number: S22687; PMID:92356824
 A:Accession: S22688
 A:Molecule type: DNA
 A:Residues: 1-129 <ALD>
 A:Cross-references: EMBL:M86530; NID:9155321; PIDN:AAD15222.1; PID:9155323
 C:Genetics:
 A:Gene: lppA
 A:Genome: plasmid

Query Match 83.3%; Score 5; DB 2; Length 129;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVD 5
 |||||
 Db 3 RKLVD 7

RESULT 13

S59643
 Hypothetical protein SPAC13C5.06c - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 10-Dec-1999
 C:Accession: S59643; T37619
 R:Devlin, K.; Churcher, C.M.
 submitted to the EMBL Data Library, July 1995
 A:Reference number: S58093
 A:Accession: S59643
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-177 <DEV>
 A:Cross-references: EMBL:Z50112; NID:908889; PIDN:CA090457.1; PID:908895
 R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, July 1995
 A:Reference number: Z21731
 A:Accession: T37619
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-177 <DEV>
 A:Molecule type: DNA
 A:Residues: 1-177 <DE2>
 A:Cross-references: EMBL:Z50112; PIDN:CA090457.1; GSPDB:GN00066; SPDB:SPAC13C5.06c
 A:Experimental source: strain 972h; cosmid c13C5
 C:Genetics:
 A:Gene: SPDB:SPAC13C5.06c
 A:Map position: 1
 A:Insertions: 76/1
 C:Superfamily: Schizosaccharomyces SPAC13C5.06c

Query Match 83.3%; Score 5; DB 2; Length 177;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKLVD 6
 |||||
 Db 70 RKLVD 74

RESULT 14

A64477
 L-fucose-phosphate aldolase homolog - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
 C:Accession: A64477
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
 Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Noese
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
 A:Reference number: A64400; PMID:96337999
 A:Accession: A64477

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-181 <BU1>
A:Cross-references: GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99428.1; PID:g1592067; T
C:Genetics:
A:Map position: FOR1381152-1381697
C:Superfamily: L-ribulose-phosphate 4-epimerase

Query Match 83.3%; Score 5; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVD 5
|||||
Db 11 RKLVD 15

RESULT 15
T47984

hypothetical protein F21F14.90 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-May-2000

C:Accession: T47984

R:Choisne, N.; Robert, C.; Brotlier, P.; Wincker, P.; Catolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, February 2000

A:Reference number: Z24481

A:Accession: T47984

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-187 <CHO>

A:Cross-references: EMBL:AL138642

A:Experimental source: cultivar Columbia; BAC clone F21F14

C:Genetics:
A:Map position: 3
A:Note: F21F14.90
C:Superfamily: Arabidopsis thaliana hypothetical protein F21F14.90

Query Match 83.3%; Score 5; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 56;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLVD 5
|||||
Db 13 RKLVD 17

Search completed: November 8, 2002, 09:38:01
Job time : 17 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:34:56 : Search time 11 Seconds
(Without alignments)
21.120 Million cell updates/sec

Title: US-09-657-431-11
Perfect score: 6
Sequence: 1 RKLXDY 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	810	1 PLMN_HUMAN	P00747 homo sapien
2	6	100.0	812	1 PLMN_MOUSE	P20918 mus musculu
3	5	83.3	112	1 IPSG_PANLE	P08481 panthera le
4	5	83.3	129	1 IPGA_SHIFL	P33547 shigella fl
5	5	83.3	177	1 YAL6_SCHPO	Q09688 schizosacch
6	5	83.3	181	1 YE18_METUA	Q58813 methanococc
7	5	83.3	190	1 RL5_METUA	P54040 methanococc
8	5	83.3	266	1 YG54_YEAST	P46947 saccharomyc
9	5	83.3	289	1 RIPS_TRIKI	P24478 trichosanth
10	5	83.3	289	1 RPLT_TRIKI	P09969 trichosanth
11	5	83.3	302	1 RRML_DROME	Q9VEP1 drosophila
12	5	83.3	305	1 DDL_BACHD	Q9KCT0 bacillus ha
13	5	83.3	368	1 DNU2_XYLEA	Q9PB06 xylella fas
14	5	83.3	376	1 DNU2_AQUAE	O66921 aquifex aeo
15	5	83.3	376	1 HIS8_SUSO	O33770 sulfolobus
16	5	83.3	379	1 PSI_SCHPO	O09912 schizosacch
17	5	83.3	387	1 YRS8_CAREL	Q10004 caenorhabdi
18	5	83.3	389	1 DNU2_MYGE	P47265 mycoplasma
19	5	83.3	405	1 DCD4_HELPJ	Q9ZM55 heliobacte
20	5	83.3	405	1 DCD4_HELPJ	Q9ZM55 heliobacte
21	5	83.3	458	1 ERR3_HUMAN	O75454 homo sapien
22	5	83.3	488	1 EXON_HSV6U	P52447 human herpe
23	5	83.3	488	1 EXON_HSV6U	P52447 human herpe
24	5	83.3	525	1 DIMH_CAREL	O17387 human herpe
25	5	83.3	527	1 YBIP_ECOLI	P75785 caenorhabdi
26	5	83.3	592	1 VP3_ROTPO	P61825 porcinia rot
27	5	83.3	974	1 CC15_YEAST	P27656 saccharomyc
28	5	83.3	1161	1 RPO2_FOPPV	O91544 fowlopox vir
29	5	83.3	1174	1 ZO2_CANFA	O95168 canis fami1
30	5	83.3	1193	1 ACE_CHICK	Q10751 gallus gall
31	5	83.3	1337	1 P152_YEAST	P39665 saccharomyc
32	5	83.3	2022	1 ANTI1_ONCVO	P21249 onchocerca
33	5	83.3	3951	1 VGFI_LBVB	P27920 avian infec

ALIGNMENTS

RESULT 1	PLMN_HUMAN	STANDARD:	PRT:	810 AA.
AC	P00747;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-MAR-1989 (Rel. 10, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Plasminogen precursor (EC 3.4.21.7) [contains: Angiostatin].			
GN	PLG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90202879; PubMed=2318848;			
RA	Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;			
RT	"Characterization of the gene for human plasminogen, a key proenzyme			
RT	in the fibrinolytic system.";			
RL	J. Biol. Chem. 265:6104-6111(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87162490; PubMed=3030813;			
RA	Forsgren M., Raden B., Israelsson M., Larsson K., Heden L.-O.;			
RT	"Molecular cloning and characterization of a full-length cDNA clone			
RT	for human plasminogen.";			
RL	FEBS Lett. 213:254-260(1987).			
RN	[3]			
RP	SEQUENCE OF 20-810.			
RA	Sottrop-Jensen L., Petersen T.E., Magnusson S.;			
RT	Submitted (JUL-1977) to the PIR data bank.			
RN	[4]			
RP	SEQUENCE OF 292-810 FROM N.A.			
RX	MEDLINE=85023311; PubMed=6148961;			
RA	Malinowski D.P., Sadler J.E., Davie E.W.;			
RT	"Characterization of a complementary deoxyribonucleic acid coding for			
RT	human and bovine plasminogen.";			
RL	Biochemistry 23:4243-4250(1984).			
RN	[5]			
RP	SEQUENCE OF 20-100.			
RX	MEDLINE=75093329; PubMed=122932;			
RA	Wiman B., Wallen P.;			
RT	"Structural relationship between 'glutamic acid' and 'lysine' forms			
RT	of human plasminogen and their interaction with the NH2-terminal			
RT	activation peptide as studied by affinity chromatography.";			
RL	Bur. J. Biochem. 50:489-494(1975).			
RN	[6]			
RP	SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810.			
RA	Sottrop-Jensen L., Claeys H., Zajdel M., Petersen T.E., Magnusson S.;			
RT	(in) Davidson J.F., Roman R.M., Samama M.M., Desnoyers P.C. (eds.);			
RT	Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,			
RL	Raven Press, New York (1978).			
RN	[7]			
RP	SEQUENCE OF 483-604.			
RX	MEDLINE=76043692; PubMed=126863;			
RA	Wiman B., Wallen P.;			

34	4	66.7	45	1	RIP2_TRIKI	P23029 trichosanth
35	4	66.7	45	1	Y00D_BPTA	O01434 bacteriopho
36	4	66.7	46	1	LHA1_ECOTHO	P80100 ecotliotho
37	4	66.7	52	1	MAHO_PSEPU	O51946 pseudomonas
38	4	66.7	62	1	TS24_DENNA	P01407 dendroaspis
39	4	66.7	62	1	TS81_DENAN	P01410 dendroaspis
40	4	66.7	62	1	TS82_DENAN	P01411 dendroaspis
41	4	66.7	63	1	TS91_DENAN	P01408 dendroaspis
42	4	66.7	63	1	TS92_DENAN	P01409 dendroaspis
43	4	66.7	67	1	YMOA_YERPE	P27720 yersinia pe
44	4	66.7	71	1	YAAA_BACSU	P05650 bacillus su
45	4	66.7	71	1	YDGT_ECOLI	P76179 escherichia

RT "Amino-acid sequence of the cyanogen-bromide fragment from human
RT plasminogen that forms the linkage between the plasmin chains.";
RL Eur. J. Biochem. 58:539-547(1975).
RN [8]
RP SEQUENCE OF 581-810.
RX MEDLINE-77225245; PubMed-142009;
RA Wiman B.;
RT "Primary structure of the B-chain of human plasmin.";
RL Eur. J. Biochem. 76:129-137(1977).
RN [9]
RP ACTIVE SITE.
RX MEDLINE-73149248; PubMed-4694729;
RA Robbins K.C., Bernabe P., Arzadon L., Summaria L.;
RT "The primary structure of human plasminogen. II. The histidine loop
RT of human plasmin: light (B) chain active center histidine sequence.";
RL J. Biol. Chem. 248:1631-1633(1973).
RN [10]
RP ACTIVE SITE.
RX MEDLINE-69234739; PubMed-4240117;
RA Groskopf W.R., Summaria L., Robbins K.C.;
RT "Studies on the active center of human plasmin. Partial amino acid
RT sequence of a peptide containing the active center serine residue.";
RL J. Biol. Chem. 244:3590-3597(1969).
RN [11]
RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RX MEDLINE-82213905; PubMed-6919539;
RA Trexler M., Valli Z., Pathy L.;
RT "Structure of the omega-aminocarboxylic acid-binding sites of human
RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
RT binding of ligand by kringle 4.";
RL J. Biol. Chem. 257:7401-7406(1982).
RN [12]
RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RX MEDLINE-85054794; PubMed-6094526;
RA Valli Z., Pathy L.;
RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
RT are essential for fibrin affinity of the kringle 1 domain.";
RL J. Biol. Chem. 259:13690-13694(1984).
RN [13]
RP PHOSPHORYLATION SITE SER-597.
RX MEDLINE-97345939; PubMed-9201958;
RA Wang H., Protok M., Brethauer R.K., Castellino F.J.;
RT "Serine-578 is a major phosphorylation locus in human plasma
RT plasminogen.";
RL Biochemistry 36:8100-8106(1997).
RN [14]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE-88185329; PubMed-3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63(1988).
RN [15]
RP CARBOHYDRATE-LINKAGE SITE 268.
RX MEDLINE-97207306; PubMed-9054441;
RA Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,
RA Pizzo S.V.;
RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
RT human plasminogen 2.";
RL J. Biol. Chem. 272:7408-7411(1997).
RN [16]
RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RX MEDLINE-95042728; PubMed-7525077;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma.";
RL Cell 79:315-328(1994).
RN [17]
RP CHARACTERIZATION OF ANGIOSTATIN.
RX MEDLINE-97238710; PubMed-9102221;
RN [18]
RP SLIM B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
RA Lapcevich R., Nacy C.A.;
RT "A recombinant human angiostatin protein inhibits experimental primary
RT and metastatic cancer.";
RL Cancer Res. 57:1329-1334(1997).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RX MEDLINE-92031502; PubMed-1657148;
RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
RT "Crystal and molecular structure of human plasminogen kringle 4
RT refined at 1.9 Å resolution.";
RL Biochemistry 30:10576-10588(1991).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RX MEDLINE-92031503; PubMed-1657149;
RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of
RT human plasminogen kringle 4.";
RL Biochemistry 30:10589-10594(1991).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RX Stec B., Yamano A., Whitlow M., Teeter M.M.;
RT Submitted (JUN-1995) to the PDB data bank.
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
RX MEDLINE-96180681; PubMed-8611560;
RA Mathews I.I., Vanderhoff-Hanaver P., Castellino F.J., Tulinsky A.;
RT "Crystal structures of the recombinant kringle 1 domain of human
RT plasminogen in complexes with the ligands epsilon-aminocaproic acid
RT and trans-4-(aminomethyl)cyclohexane-1-carboxylic acid.";
RL Biochemistry 35:2567-2576(1996).
RN [23]
RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
RX MEDLINE-98198034; PubMed-9521645;
RA Chang Y., Mochalkin I., Mccance S.G., Cheng B., Tulinsky A.,
RA Castellino F.J.;
RT "Structure and ligand binding determinants of the recombinant kringle
RT 5 domain of human plasminogen.";
RL Biochemistry 37:3258-3271(1998).
RN [24]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE-94237157; PubMed-8181475;
RA Rejzante M.R., Llinas M.;
RT "1H-NMR assignments and secondary structure of human plasminogen
RT kringle 1.";
RL Eur. J. Biochem. 221:927-937(1994).
RN [25]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE-94237158; PubMed-8181476;
RA Rejzante M.R., Llinas M.;
RT "Solution structure of the epsilon-aminohexanoic acid complex of
RT human plasminogen kringle 1.";
RL Eur. J. Biochem. 221:939-949(1994).
RN [26]
RP STRUCTURE BY NMR OF 183-354.
RX MEDLINE-96194156; PubMed-8652577;
RA Soehndel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
RA Rickli E.E.;
RT "Recombinant gene expression and 1H NMR characteristics of the
RT kringle (2 + 3) supermodule: spectroscopic/functional individuality
RT of plasminogen kringle domains.";
RL Biochemistry 35:2357-2364(1996).
RN [27]
RP VARIANTS PHE-374 AND THR-620.
RX MEDLINE-91095410; PubMed-1986355;
RA Ichinose A., Espling E.S., Takamatsu J., Saito H., Shimoyozu K.,

Query Match 100.0%; Score 6; DB 1; Length 810;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RKLXY 6
 |||||
 Db 549 RKLXY 554

RESULT 2

PLAN_MOUSE STANDARD; PRT; 812 AA.
 AC P20918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
 GN Plg.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91184812; PubMed=2081600;
 RA Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
 RT "Characterization of the cDNA coding for mouse plasminogen and
 RL localization of the gene to mouse chromosome 17.";
 RL Genomics 8:49-61(1990).
 RN [2]
 RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
 RX MEDLINE=95042728; PubMed=7525077;
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
 RL suppression of metastases by a Lewis lung carcinoma.";
 RL Cell 79:315-328(1994).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
 NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
 METASTATIC TUMORS IN VIVO.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
 INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD
 TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
 ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPsin FAMILY. PLASMINOGEN SUBFAMILY.
 CC -----
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 DR EMBL; J04766; AAA50168.1; -;
 DR PIR; A38514; A38514.
 DR HSSP; P00747; 1PMK.

DR MEROPS; S01.233; -;
 DR MGD; MG1:97620; Plg.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR01254; Trypsin.
 DR Pfam: PF00051; kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPsin.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS0070; KRINGLE_2; 5.
 DR PROSITE; PS0240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 DR HydroLase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 812
 FT CHAIN 20 581
 FT PEPTIDE 20 97
 FT CHAIN 98 581
 FT CHAIN 98 7436
 FT CHAIN 582 812
 FT CHAIN 582 181
 FT DOMAIN 103 181
 FT DOMAIN 184 262
 FT DOMAIN 275 352
 FT DOMAIN 377 454
 FT DOMAIN 481 560
 FT DOMAIN 582 812
 FT ACT_SITE 624 624
 FT ACT_SITE 667 667
 FT ACT_SITE 762 762
 FT DISULFID 49 73
 FT DISULFID 53 61
 FT DISULFID 103 181
 FT DISULFID 124 164
 FT DISULFID 152 176
 FT DISULFID 185 262
 FT DISULFID 188 316
 FT DISULFID 206 245
 FT DISULFID 234 257
 FT DISULFID 275 352
 FT DISULFID 296 335
 FT DISULFID 324 347
 FT DISULFID 377 454
 FT DISULFID 398 437
 FT DISULFID 426 449
 FT DISULFID 481 560
 FT DISULFID 502 543
 FT DISULFID 531 555
 FT DISULFID 568 687
 FT DISULFID 578 586
 FT DISULFID 609 625
 FT DISULFID 701 768
 FT DISULFID 731 747
 FT DISULFID 758 786
 SQ SEQUENCE 812 AA; 90846 MW; D34A74A4FC2256F8 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 812;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RKLXY 6
 |||||
 Db 549 RKLXY 554

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RESULT 3
IPSG_PANLE STANDARD: PRT: 112 AA.
ID IPSG_PANLE
AC P08481:
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Double-headed protease inhibitor, submandibular gland.
OS Panthera leo (Lion).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
OC NCBI_TaxID=9689;
RN [1]
RC SEQUENCE.
RP TISSUE=Submandibular gland;
RX MEDLINE=87299011; PubMed=3304339;
RA Reisinger P.W.M., Hochstrasser K., Gottlicher I., Eultz M.,
RA Wachter E.;
RT "The amino-acid sequences of the double-headed proteinase inhibitors
RT from cat, lion and dog submandibular glands.";
RL Biol. Chem. Hoppe-Seyler 368:717-726(1987).
CC -1- FUNCTION: THIS INHIBITOR IS COMPOSED OF TWO HOMOLOGOUS ACTIVELY
CC INHIBITING HALVES: ONE WHICH INHIBITS TRYPSIN, THE OTHER WHICH
CC INHIBITS ELASTASE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: CONTAINS 2 KAZAL-LIKE DOMAINS.
DR HSSP: P05586; 40NO.
DR InterPro: IPR001239; Kazal_inhib.
DR InterPro: IPR002350; Kazal.
DR Pfam: PF00050; Kazal_2.
DR PRINTS: PR00290; KAZALINHTR.
DR SMART: SM00280; KAZAL_2.
DR PROSITE: PS00282; KAZAL: 2.
KW Serine protease inhibitor; Repeat; Submandibular gland.
FT DOMAIN 1 60 KAZAL-LIKE 1.
FT ACT_SITE 22 23 REACTIVE BOND 1 (TRYPSIN).
FT ACT_SITE 73 74 REACTIVE BOND 2 (ELASTASE).
FT DISULFID 8 42 BY SIMILARITY.
FT DISULFID 20 39 BY SIMILARITY.
FT DISULFID 28 60 BY SIMILARITY.
FT DISULFID 64 93 BY SIMILARITY.
FT DISULFID 71 90 BY SIMILARITY.
FT DISULFID 79 111 BY SIMILARITY.
SQ SEQUENCE 112 AA; 12740 MW; D8062796D3FC611C CRC64;

Query Match 83.3%; Score 5; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVD 5
DB 53 RKLVD 57

RESULT 4
IPGA_SHIFL STANDARD: PRT: 129 AA.
ID IPGA_SHIFL
AC P33547;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Igpa protein.
OS Shigella flexneri.
OC Plasmid 210 kb invasion pWR100.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
OC NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T / SEROTYPE 5;

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RX MEDLINE=92356824; PubMed=1495389;
RA Aliaoui A., Mounier J., Prevost M.-C., Sansonetti P.J., Parsot C.;
RT "IcsB: a Shigella flexneri virulence gene necessary for the lysis of
RT protrusions during intercellular spread.";
RL Mol. Microbiol. 6:1605-1616(1992).
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CC -----
DR EMBL: M86530; AAD15222.1; -
DR PTR: S22688; S22688.
KW Plasmid; Virulence.
SQ SEQUENCE 129 AA; 15085 MW; 8780F58428A78847 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVD 5
DB 3 RKLVD 7

RESULT 5
YA16_SCHPO STANDARD: PRT: 177 AA.
ID YA16_SCHPO
AC Q09688;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical 20.1 kDa protein C13C5.06c in chromosome I precursor.
GN SPAC13C5.06c.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: Z50112; CAA90457.1; -
KW Hypothetical protein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 177 HYPOTHETICAL PROTEIN C13C5.06c.
FT CARBOHYD 121 121 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 177 AA; 20058 MW; 612DE3D3F7B64027 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLYVD 6
DB 70 KLYVD 74

RESULT 6

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YE18_METJA STANDARD; PRT; 181 AA.
ID YE18_METJA
AC O58813;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical aldolase class II protein MJ1418.
GN MJ1418.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ANAD/FUCA
CC -1- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC SOBEFAMILY. STRONG, TO E.COLI YGBL AND H.INFLUENZAE HI1012.
CC
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DR EMBL: U67582; AAB9428.1; -.
DR HSP: P11550; 3FUA.
DR TIGR: MJ1418; -.
DR InterPro: IPR001303; Aldolase-II.
DR Pfam: PF00596; Aldolase-II; 1.
KW Hypothetical protein; zinc; Complete proteome.
FT METAL 68 68 ZINC (BY SIMILARITY).
FT METAL 87 87 ZINC (BY SIMILARITY).
FT METAL 89 89 ZINC (BY SIMILARITY).
FT METAL 147 147 ZINC (BY SIMILARITY).
SQ SEQUENCE 181 AA; 20470 MW; E5F3BF13722145B0 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKLVD 5
DB 11 RKLVD 15

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RN
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS.
CC
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DR EMBL: U67497; AAB98458.1; -.
DR TIGR: MJ0469; -.
DR InterPro: IPR002132; Ribosomal_L5.
DR Pfam: PF00281; Ribosomal_L5; 1.
DR PROSITE: PS00673; Ribosomal_L5_C; 1.
DR PROSITE: PS00358; Ribosomal_L5; 1.
DR PROSITE: PS00358; RIBOSOMAL_L5; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 190 AA; 22169 MW; BD0536973C3A533 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KLYDY 6
DB 96 KLYDY 100

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RESULT 7
ID RLS_METJA STANDARD; PRT; 190 AA.
AC P54040;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L5P.
GN RPL5P OR MJ0469.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;

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RESULT 8
ID YGS4_YEAST STANDARD; PRT; 266 AA.
AC P46947;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 30.5 kDa protein in SAE2-KEM1 intergenic region.
GN YGL174W OR G1642.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=96109931; PubMed=8619317;
RA Bertani I., Cogoli V., Zaccaria P., Klima R., Bruschi C.V.;
RT "The sequence of an 11.1 kb fragment on the left arm of Saccharomyces
cerevisiae chromosome VII reveals six open reading frames including
NSP49, KEM1 and four putative new genes."
RL Yeast 11:1187-1194(1995).
CC -1- SIMILARITY: SOME, TO C.ELEGANS R08D7.1.
CC
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DR EMBL: X84705; CAA59179.1; -
 DR EMBL: 272696; CAA96886.1; -
 DR SGD: S0003142; YGL174W.
 KW Hypothetical protein.
 SQ SEQUENCE 266 AA; 30472 MW; 1564B390121325CD CRC64;

Query Match 83.3%; Score 5; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYD 5
 Db 212 RKLYD 216

RESULT 9

RIPS_TRIKI STANDARD; PRT; 289 AA.

AC P24478;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein karasurin precursor (rRNA
 N-glycosidase) (EC 3.2.2.22).
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Root tuber;
 RA MEDLINE=97356562; PubMed=9212998;
 RA Mizukami H., Iida K., Kondo T., Ogihara Y.;
 RT "Cloning and bacterial expression of a gene encoding ribosome-
 inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
 kirilowii var. japonica";
 RT Biol. Pharm. Bull. 20:711-713(1997).
 RN [2]
 RP SEQUENCE OF 24-270.
 RX MEDLINE=92005921; PubMed=1914000;
 RA Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
 RT "The complete amino acid sequence of an abortifacient protein,
 karasurin";
 RL Chem. Pharm. Bull. 39:1244-1249(1991).
 CC -1- FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES EUKARYOTIC
 CC 60S RIBOSOMAL SUBUNITS.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY, TYPE 1
 CC RIP SUBFAMILY.

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DR EMBL: AB000666; BAA21786.1; -
 DR PIR: J00393; J00393.
 DR HSSP: P09989; IMRJ.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 KW Antiviral; Protein synthesis inhibitor; Hydrolase; Toxin; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 270 KARASURIN-C.

FT CHAIN 24 270 KARASURIN-A.
 FT PROPEP 271 289 REMOVED IN NATURE FORM.
 FT ACT_SITE 183 183 BY SIMILARITY.
 SQ SEQUENCE 289 AA; 31704 MW; 883D3E3242887B26 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYD 5
 Db 52 RKLYD 56

RESULT 10

RIP_TRIKI STANDARD; PRT; 289 AA.

AC P09989;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein alpha-trichosanthin precursor
 (rRNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAXIMOWICZ;
 RX MEDLINE=91153657; PubMed=1999291;
 RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
 RT "Cloning of trichosanthin cDNA and its expression in Escherichia
 coli";
 RT Gene 97:267-272(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAXIMOWICZ; TISSUE=leaf;
 RX MEDLINE=90256790; PubMed=2341400;
 RA Chow T., Feldman R.A., Lovett M., Platek M.;
 RT "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a
 RT type I ribosome-inactivating protein";
 RL J. Biol. Chem. 265:8670-8674(1990).
 RN [3]
 RP SEQUENCE OF 24-270.
 RC STRAIN=MAXIMOWICZ; TISSUE=tuberous root;
 RX MEDLINE=90256789; PubMed=2341399;
 RA Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
 RA Wu P., Hwang K., Platek M.;
 RT "Primary amino acid sequence of alpha-trichosanthin and molecular
 RT models for abrin A chain and alpha-trichosanthin";
 RL J. Biol. Chem. 265:8665-8669(1990).
 RN [4]
 RP SEQUENCE OF 24-270.
 RC TISSUE=tuberous root;
 RA Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
 RA Tian G.Y., Ni C.Z.;
 RT "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and
 RT application";
 RL Pure Appl. Chem. 58:789-798(1986).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
 RX MEDLINE=94344957; PubMed=8066085;
 RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;
 RT "Structure of trichosanthin at 1.88-A resolution";
 RL Proteins 19:4-13(1994).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=95344383; PubMed=7619070;
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
 RT "Studies on crystal structures, active-centre geometry and
 RT depurinating mechanism of two ribosome-inactivating proteins";

RL Biochem. J. 309:285-298(1995).
 CC -1- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
 CC CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT
 CC INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY. TYPE 1
 CC RIB SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: M34858; AAA34207.1; -;
 DR EMBL: J05434; AAA34206.1; -;
 DR PIR: J70003; RLRTZ.
 DR PIR: J70566; J70566.
 DR PIR: A36273; A36273.
 DR PIR: A36274; A36274.
 DR PDB: 1MRJ; 07-FEB-95.
 DR PDB: 1MRK; 07-FEB-95.
 DR PDB: 1TCS; 10-JUL-95.
 DR InterPro: IPR001574; RLP.
 DR Pfam: PF00161; RLP.
 DR PRINTS: PR00396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGARICIN.
 KW Antiviral; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
 KW 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 270
 FT PROPEP 271 289
 FT ACT_SITE 183 183
 FT CONFLICT 57 60
 FT CONFLICT 82 84
 FT CONFLICT 87 87
 FT CONFLICT 92 92
 FT CONFLICT 143 144
 FT CONFLICT 196 196
 FT CONFLICT 214 216
 FT CONFLICT 231 231
 FT CONFLICT 234 234
 FT CONFLICT 246 266
 FT CONFLICT 247 247
 FT SEQUENCE 289 AA; 31676 MW; 5CE09B8630575BB9 CRC64;
 Query Match 83.3%; Score 5; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKLVD 5
 Db 52 RKLVD 56
 RESULT 11
 RRM1_DROME STANDARD; PRT; 302 AA.
 AC Q9VEP1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative ribosomal RNA methyltransferase CG5220 (EC 2.1.1.-) (rRNA
 DE (uridine-2'-O)-methyltransferase).
 GN CG5220.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidae; Drosophilidae; Drosophila.

OX NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blaise R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei L., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT The genome sequence of Drosophila melanogaster.;
 RL Science 287:2185-2195(2000).
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + RNA = S-ADENOSYL-L-
 CC HOMOCYSTEINE + RNA CONTAINING 2'-O-METHYLURIDINE.
 CC -1- SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY. RRMJ
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: AE003716; AAF55380.1; -;
 DR FlyBase: FBgn0038471; CG5220.
 DR InterPro: IPR002877; FtsJ.
 DR Pfam: PF01728; FtsJ; 1.
 KW Hypothetical protein; rRNA processing; Transferase; Methyltransferase.
 SQ SEQUENCE 302 AA; 33402 MW; EDFB3BAD445693DA CRC64;
 Query Match 83.3%; Score 5; DB 1; Length 302;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKLVD 5
 Db 61 RKLVD 65
 RESULT 12

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DDL_BACHD
ID DDL_BACHD STANDARD: PRT: 305 AA.
AC 09KCF0:
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE D-alanyl-D-alanine ligase (EC 6.3.2.4) (D-alanyltalanine synthetase)
DE (D-Ala-D-Ala ligase).
GN DDL OR DDLA OR BHI621.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86655;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: Cell wall formation (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + D-alanine + D-alanine = ADP + phosphate
CC + D-alanyl-D-alanine.
CC -1- PATHWAY: ALONG WITH ALANINE RACEMASE, IT MAKES UP THE D-ALANINE
CC -1- BRANCH OF THE PEPTIDOGLYCAN BIOSYNTHETIC ROUTE.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE D-ALANINE-D-ALANINE LIGASE FAMILY.
CC -----
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CC -----
DR EMBL: AP01512; BAB05340.1; -
DR HSSP: P07662; 110W.
DR InterPro: IPR000291; Data_Data_Ligase.
DR Pfam: PF01820; Data_Data_Ligase_2.
DR PROSITE: PS00843; DALA_DATA_LIGASE_1; 1.
DR PROSITE: PS00844; DALA_DATA_LIGASE_2; FALSE_NEG.
KW Ligase; Cell wall; Peptidoglycan synthesis; Complete proteome.
SQ SEQUENCE 305 AA; 33125 MW; C806D03993D3D081 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 305;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLYDY 6
DB 204 KLYDY 208

RESULT 13
DNAJ_XYLFA
ID DNAJ_XYLFA STANDARD: PRT: 368 AA.
AC 09PB06:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DnaJ OR XEF2339.
GN DnaJ OR XEF2339.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
FT METAL

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RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinhard F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Britons M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferio J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Ganler M., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnel J.D., Junqueira M.L., Kemper E.L., Kitaajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Onagajo R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zaitz M., Zeldanis J., Zetubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
CC -1- FUNCTION: ACTS AS A CO-CHAPERONE. STIMULATES, JOINTLY WITH GRPE,
CC THE ATPASE ACTIVITY OF DnaJ (By similarity).
CC -1- COFACTOR: BINDS TWO ZINC IONS PER MONOMER (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE DnaJ FAMILY.
CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.
CC -----
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CC -----
DR EMBL: AE004044; AAF85138.1; -
DR InterPro: IPR003095; DnaJ.
DR InterPro: IPR002939; DnaJ_C.
DR InterPro: IPR001305; DnaJ_CXXCXGXG.
DR InterPro: IPR001623; DnaJ_N.
DR Pfam: PF01556; DnaJ_C_1.
DR Pfam: PF00684; DnaJ_CXXCXGXG_1.
DR PRINTS: PR00625; DnaJPROTEIN.
DR SMART: SM00271; DnaJ_1.
DR PROSITE: PS00636; DnaJ_1; FALSE_NEG.
DR PROSITE: PS50076; DnaJ_2; 1.
DR PROSITE: PS00637; DnaJ_CXXCXGXG_1.
KW Chaperone; DNA replication; Heat shock; Repeat; zinc; Metal-binding;
KW Complete proteome.
FT METAL
FT DOMAIN 5 70
FT DOMAIN 77 111
FT REPEAT 137 144 GLY-RICH.
FT REPEAT 153 160 CXXCXGXG MOTIF.
FT REPEAT 175 182 CXXCXGXG MOTIF.
FT REPEAT 189 196 CXXCXGXG MOTIF.
FT METAL 137 137 ZINC 1 (BY SIMILARITY).
FT METAL 140 140 ZINC 1 (BY SIMILARITY).
FT METAL 153 153 ZINC 2 (BY SIMILARITY).
FT METAL 156 156 ZINC 2 (BY SIMILARITY).
FT METAL 175 175 ZINC 2 (BY SIMILARITY).
FT METAL 178 178 ZINC 2 (BY SIMILARITY).
FT METAL 189 189 ZINC 1 (BY SIMILARITY).
FT METAL 192 192 ZINC 1 (BY SIMILARITY).

```

SQ SEQUENCE 368 AA; 40372 MW; 8631363433805B9 CRC64;
 Query Match 83.3%; Score 5; DB 1; Length 368;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVD 5
 |||||
 Db 63 RKLVD 67

RESULT 14
 DNJ2_AQOAE STANDARD: PRT; 376 AA.
 AC 066921;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Chaperone protein dnaJ-2.
 GN DNJ2 OR AQ_703.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RX MEDLINE=98196666; PubMed=9537320;
 RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sned M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson N.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus.";
 RL Nature 392:353-358(1998).
 CC -1- FUNCTION: ACTS AS A CO-CHAPERONE. STIMULATES, JOINTLY WITH GRPE,
 CC THE ATPASE ACTIVITY OF DNAK (BY SIMILARITY).
 CC -1- COFACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE DNJ FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 J DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.
 CC -----
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 CC -----
 DR EMBL; AE000703; AAC06881.1; -;
 DR HSSP; P08622; 1XBL.
 DR InterPro: IPR003095; DnaJ.
 DR InterPro: IPR002939; DnaJ_C.
 DR InterPro: IPR001305; DnaJ_CXKXGXG.
 DR InterPro: IPR001623; DnaJ_N.
 DR Pfam; PF00226; DnaJ_1.
 DR Pfam; PF00556; DnaJ_C_1.
 DR Pfam; PF00684; DnaJ_CXKXGXG; 1.
 DR PRINTS; PR00625; DNAJPROTEIN.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ_1; 1.
 DR PROSITE; PS0076; DnaJ_2; 1.
 DR PROSITE; PS00637; DnaJ_CXKXGXG; FALSE NEG.
 KM Chaperone; DNA replication; Heat shock; Repeat; zinc; Metal-binding;
 KW Complete proteome.
 FT DOMAIN 8 72 J-DOMAIN.
 FT REPEAT 156 163 CXKXGXG MOTIF.
 FT REPEAT 172 179 CXKXGXG MOTIF.
 FT REPEAT 194 201 CXKXGXG MOTIF.
 FT REPEAT 207 214 CXKXGXG MOTIF.
 FT METAL 156 156 ZINC 1 (BY SIMILARITY).
 FT METAL 159 159 ZINC 1 (BY SIMILARITY).
 FT METAL 172 172 ZINC 2 (BY SIMILARITY).

FT METAL 175 175 ZINC 2 (BY SIMILARITY).
 FT METAL 194 194 ZINC 2 (BY SIMILARITY).
 FT METAL 197 197 ZINC 2 (BY SIMILARITY).
 FT METAL 207 207 ZINC 1 (BY SIMILARITY).
 FT METAL 210 210 ZINC 1 (BY SIMILARITY).
 SQ SEQUENCE 376 AA; 41963 MW; 9C8BFBF29A8A016D CRC64;
 Query Match 83.3%; Score 5; DB 1; Length 376;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVD 5
 |||||
 Db 65 RKLVD 69

RESULT 15
 HIS8_SULSO STANDARD: PRT; 376 AA.
 AC 033770;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Imidazole acetyl-
 DE phosphate transaminase).
 GN HIS8 OR SSO0592 OR C08_058.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=973522708; PubMed=9209067;
 RA Charlebois R.L., Sensen C.W., Doolittle W.F., Brown J.R.;
 RT "Evolutionary analysis of the hisGABGFDHI gene cluster from the
 RT archaeon Sulfolobus solfataricus P2.";
 RL J. Bacteriol. 179:4429-4432(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=20165948; PubMed=10701121;
 RA Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,
 RA Confalonieri F., Curtis B., Duguet M., Eranuo G., Faguy D.,
 RA Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,
 RA Kushnaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q.,
 RA St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F.,
 RA Ragan M.A., Sensen C.W.;
 RT "Gene content and organization of a 281-kbp contig from the genome of
 RT the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";
 RL Genome 43:116-136(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21332295; PubMed=11427726;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moers A., Eranuo G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 CC -1- CATALYTIC ACTIVITY: L-histidinol-phosphate + 2-oxoglutarate -> 3-
 CC (imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- PATHWAY: EIGHTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 CC -----
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CC -----
DR EMBL; U82227; AAB63018.1; -;
DR EMBL; Y18930; CAB57708.1; -;
DR EMBL; AE006689; AAK40904.1; -;
DR InterPro; IPR001511; AminoTran_1.
DR InterPro; IPR001917; AminoTran_2.
DR Pfam; PF00155; aminoTran_1_2; 1.
DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; 1.
KW Histidine biosynthesis; Transferase; AminoTransferase;
FT Pyridoxal phosphate; Complete proteome.
FT BINDING 240 PYRIDOXAL PHOSPHATE (PROBABLE).
SQ SEQUENCE 376 AA; 43193 MW; 44CAB23CD2866405 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVD 5
|||||
Db 342 RKLVD 346

Search completed: November 8, 2002, 09:37:38
Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:36:17 ; Search time 25 Seconds
(without alignments)
41.519 Million cell updates/sec

Title: US-09-657-431-11

Perfect score: 6

Sequence: 1 RKLVDY 6

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size: 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	6	334	6	046507 papio hamad
2	100.0	6	810	4	015146 homo sapien
3	100.0	6	812	11	09ROW3 ratius norv
4	100.0	6	812	11	091WJ5 mus musculu
5	83.3	5	72	16	09PR65 ureaplasm
6	83.3	5	73	2	09X3B8 pedicoccus
7	83.3	5	79	16	09ZHB1 rickettsia
8	83.3	5	104	16	09PMK4 campylobact
9	83.3	5	107	2	052124 escherichia
10	83.3	5	110	16	032180 bacillus su
11	83.3	5	111	5	09VAM7 drosophila
12	83.3	5	111	5	09VX16 drosophila
13	83.3	5	129	4	09UNJ4 homo sapien
14	83.3	5	148	16	098F36 rhizobium l
15	83.3	5	157	10	09AUJ1 oryza sativ
16	83.3	5	158	9	037913 bacterioph

17	83.3	170	2	09KX31 streptococc
18	83.3	187	10	09M273 arabidopsis
19	83.3	205	16	09PRO5 xyloella fas
20	83.3	208	10	09XGJ5 gnetum gnet
21	83.3	209	10	040702 oryza sativ
22	83.3	212	10	09AR51 zeamays (m
23	83.3	212	10	09AR50 zeamays (m
24	83.3	212	10	09AR49 zeamays (m
25	83.3	215	16	09F5P2 rhizobium m
26	83.3	231	10	065032 oryza sativ
27	83.3	231	16	09BHL6 rhizobium l
28	83.3	232	2	09ZHS1 bruceella ab
29	83.3	232	2	086246 helicobacte
30	83.3	233	16	09FDP5 rhizobium m
31	83.3	234	10	09S138 arabidopsis
32	83.3	234	10	049351 arabidopsis
33	83.3	237	2	09RNM4 rhodobacter
34	83.3	237	2	049198 mycoplasma
35	83.3	247	10	09LRE3 trichosanth
36	83.3	256	10	09LVC4 trichosanth
37	83.3	264	16	09ZK74 helicobacte
38	83.3	264	16	097H17 clostridium
39	83.3	266	2	09KX34 streptococc
40	83.3	269	5	097118 drosophila
41	83.3	277	5	09W0A8 pyrococcus
42	83.3	280	17	058194 pyrococcus
43	83.3	283	17	09UYF1 pyrococcus
44	83.3	289	10	041216 trichosanth
45	83.3	289	10	094KE4 trichosanth

ALIGNMENTS

RESULT 1
ID 046507 PRELIMINARY; PRT: 334 AA.
AC 046507;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PLASMINOGEN (FRAGMENT).
GN BABPEPSC.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Cox L.A., Jett C., Hixson J.E.;
RT "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice
RT Site Mutation is Associated with Deletion of a Single Exon in a Null
RT Allele."
RL Submitted (OCF-1997) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC EMBL: AF023692; AAB97887.1; -.
DR HSSP: P00747; 5HPG.
DR MEROPS: S01.233; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00051; Kringle; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR: 1.
DR SMART: SM00020; Tryp-Spc: 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS00070; KRINGLE_2; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.

DR PROSITE: PS00134; TRYPSIN_HIS; 1.
KW Hydrolase; Serine protease.
FT NON_TER 1
SQ SEQUENCE 334 AA; 36791 MW; C7DC06E03B965286 CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 6; Length 334;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVDY 6
|||||
Db 73 RKLVDY 78

RESULT 2
ID 015146 PRELIMINARY; PRT; 810 AA.
AC 015146;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PLASMINOGEN PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
RA Mitchell D., Robinson J.H.;
RT "Expression of recombinant human plasminogen and alycoplasminogen in
RT HeLa cells.";
RT Fibrinolysis 0:0-0(1991).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: M74220; AAA36451.1; -.
DR HSSP: P00747; 2PK4.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan.app.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00051; Kringle; 5.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR; 5.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00021; KRINGLE_1; 5.
DR PROSITE: PS50070; KRINGLE_2; 5.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal.
FT SIGNAL 1
FT CHAIN 20 810 POTENTIAL.
SQ SEQUENCE 810 AA; 90555 MW; B05C7D4B0D020B3C CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 4; Length 810;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVDY 6
|||||
Db 549 RKLVDY 554

RESULT 3
Q9R0W3

ID Q9R0W3 PRELIMINARY; PRT; 812 AA.
AC Q9R0W3;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PLASMINOGEN PROTEIN PRECURSOR (EC 3.4.21.7).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid-10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Bangert K., Johnsen A.H., Thorsen S.;
RT "Rat plasminogen: cDNA and gene structure";
RT Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE-91250378; PubMed-1645711;
RA Kanalas J.J., Makker S.P.;
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
RT receptor site for plasminogen.";
RT J. Biol. Chem. 266:10825-10829(1991).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY

DR EMBL: AJ242649; CAP46014.1; -.
DR HSSP: P00747; IPWK.
DR MEROPS: S01.233; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan.app.
DR InterPro: IPR001400; SOMATOTROPIN.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00051; Kringle; 5.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR; 4.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00021; KRINGLE_1; 5.
DR PROSITE: PS50070; KRINGLE_2; 5.
DR PROSITE: PS50240; SOMATOTROPIN_2; UNKNOWN_1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal.
FT SIGNAL 1
FT CHAIN 20 812 PLASMINOGEN.
SQ SEQUENCE 812 AA; 90535 MW; 8C703C51410EBC9E CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 11; Length 812;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVDY 6
|||||
Db 549 RKLVDY 554

RESULT 4
ID Q91WU5 PRELIMINARY; PRT; 812 AA.
AC Q91WU5;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PLASMINOGEN.
OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC014773; AAL14773.1; -;
 SQ SEQUENCE 812 AA; 90781 MW; 24173260E6A2FFD2 CRC64;

Query Match 100.0%; Score 6; DB 11; Length 812;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLVD 6
 |||||
 DB 549 RKLVD 554

RESULT 5

O9PR65 PRELIMINARY; PRT; 72 AA.
 AC O9PR65;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, last annotation update)
 DE HYPOTHETICAL PROTEIN UU080.
 GN UU080.
 OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Ureaplasma.
 OX NCBI_TaxID=134821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROVAR 3;
 RX MEDLINE=20500219; PubMed=11048724;
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
 RA Cassell G.H.;
 RT "The complete sequence of the mucosal pathogen Ureaplasma
 RT urealyticum";
 RL Nature 407:757-762(2000).
 DR EMBL; AE002107; AAF30485.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 72 AA; 8562 MW; 5DFD61B9A9554B7 CRC64;

Query Match 83.3%; Score 5; DB 16; Length 72;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLVD 5
 |||||
 DB 50 RKLVD 54

RESULT 6

O9X3B8 PRELIMINARY; PRT; 73 AA.
 AC O9X3B8;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, last annotation update)
 DE ORF7.
 OS Pedicoccus pentosaceus.
 OC Plasmid pMD136.
 OG Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
 OC Pedicoccus.
 OX NCBI_TaxID=1255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC43200;
 RA Kantor A., Mett A., Shapira R.;
 RT "Pedicoccus pentosaceus pediocin A encoding plasmid, pMD136.";

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC43200;
 RA Giacomini A., Squartini A., Nuti M.P.;
 RT "Nucleotide sequence and analysis of plasmid pMD136 from *Pedi-* *ococcus*
 RT *pentosaceus* FB861 (ATCC43200) involved in *Pediocin A* production.";
 RL Plasmid 0:0-0(2000).
 DR EMBL; AF069302; AAD25913.1; -;
 DR EMBL; AF033858; AAF22854.1; -;
 KW Plasmid; Hypothetical protein.
 SQ SEQUENCE 73 AA; 8526 MW; 16277C452C104897 CRC64;

Query Match 83.3%; Score 5; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLVD 5
 |||||
 DB 47 RKLVD 51

RESULT 7

O92HB1 PRELIMINARY; PRT; 79 AA.
 AC O92HB1;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE ANKYRIN LIKE PROTEIN.
 GN RC0860.
 OS Rickettsia conorii.
 CC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MALISH 7;
 RX MEDLINE=21442074; PubMed=11557893;
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-F., Barbe V.,
 RA Sanson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";
 RL Science 293:2093-2098(2001).
 DR EMBL; AF008641; AAL03398.1; -;
 KW Complete proteome.
 SQ SEQUENCE 79 AA; 9340 MW; FEA9F7581A040ED2 CRC64;

Query Match 83.3%; Score 5; DB 16; Length 79;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLVD 5
 |||||
 DB 21 RKLVD 25

RESULT 8

O9PMK4 PRELIMINARY; PRT; 104 AA.
 AC O9PMK4;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE PUTATIVE PERIPLASMIC PROTEIN.
 GN CJI456C.
 OS Campylobacter jejuni.
 CC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 OC Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NCTC 11168;

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RX MEDLINE=20150912; PubMed=10688204;
RA Parthill J., Wren B.W., Mungall K., Kelley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagsals K., Kallayshv A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajadream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrett B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000)
DR EMBL: AL139078; CAB73879.1; -
KW Complete proteome.
SQ SEQUENCE 104 AA; 11853 MW; BE26E94537C791B8 CRC64;

Query Match
Best Local Similarity 83.3%; Score 5; DB 16; Length 104;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKLVD 6
DB 53 RKLVD 57

RESULT 9
ID 052124 PRELIMINARY; PRT; 107 AA.
AC 052124;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HYPOHETICAL. 12.3 KDA PROTEIN L0052 (ORF3).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98254123; PubMed=9593291;
RA Elliott S.J., Mainwright L.A., McDaniell T.K., Jarvis K.G., Deng Y.K.,
RA Lai L.C., McNamara B.P., Donenberg M.S., Kaper J.B.;
RT "The complete sequence of the locus of enterocyte effacement (LEE)
RT from enteropathogenic Escherichia coli E2348/69."
RL Mol. Microbiol. 28:1-4(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=EDL933;
RX MEDLINE=98339885; PubMed=9673266;
RA Perna N.T., Mayhew G.F., Postel G., Elliott S., Donenberg M.S.,
RA Kaper J.B., Blattner F.R.;
RT "Molecular evolution of a pathogenicity island from enterohemorrhagic
RT Escherichia coli O157:H7."
RL Infect. Immun. 66:3810-3817(1998).
DR EMBL: AF022236; AAC38366.1; -
DR EMBL: AF071034; AAC31531.1; -
KW Hypothetical protein.
SQ SEQUENCE 107 AA; 12298 MW; 9B3FFBAC8D446CE CRC64;

Query Match
Best Local Similarity 83.3%; Score 5; DB 2; Length 107;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVD 5
DB 68 RKLVD 72

RESULT 10
ID 032180 PRELIMINARY; PRT; 110 AA.
AC 032180;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE YGSN PROTEIN.

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GN YGSN.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.U., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Eutlin K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Filiz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Hatach J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandendol M., Vannier F., Vassartotti A.,
RA Viari A., Wambolt R., Wedler E., Wedler H., Wellzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: 299120; CAB15275.1; -
DR InterPro: IPR000130; Zn_MTPepidase.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 110 AA; 13138 MW; 17FE812FBE408253 CRC64;

Query Match
Best Local Similarity 83.3%; Score 5; DB 16; Length 110;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVD 5
DB 69 RKLVD 73

RESULT 11
ID 09VAV7 PRELIMINARY; PRT; 111 AA.
AC 09VAV7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CG17856 PROTEIN.
GN CG17856.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

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OX NCBI_TaxID=7227;
RN
RN SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck D., Brinkstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003764; AAF56781.1;
DR FlyBase; FBgn0039576; CG17856.
DR InterPro; IPR003197; UCR_14KD.
DR Pfam; PF02271; UCR_14KD.1.
DR Hypothetical protein.
SQ SEQUENCE 111 AA; 13517 MW; 839BE06F2E1B05D7 CRC64;

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Query Match 83.3%; Score 5; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 RKLVD 5
Db 52 RKLVD 56

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RESULT 12
Q9VX16 PRELIMINARY; PRT; 111 AA.
AC Q9VX16;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE CG3560 PROTEIN.
GN
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Diptera; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck D., Brinkstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003501; AAF48576.1;
DR FlyBase; FBgn0030733; CG3560.
DR InterPro; IPR003197; UCR_14KD.
DR Pfam; PF02271; UCR_14KD.1.
DR Hypothetical protein.
SQ SEQUENCE 111 AA; 13568 MW; 17E80E542F454624 CRC64;

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Query Match 83.3%; Score 5; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 RKLVD 5
Db 52 RKLVD 56

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RESULT 13
Q9UNJ4 PRELIMINARY; PRT; 129 AA.
AC Q9UNJ4;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE ESTROGEN RECEPTOR RELATED PROTEIN 3 (FRAGMENT).
GN ESR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;

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RX MEDLINE=99357798; PubMed=10428842;
RA Hong H., Yang L., Stallcup M.R.;
RT "Hormone-independent transcriptional activation and coactivator
RT binding by novel orphan nuclear receptor ERK3.";
RL J. Biol. Chem. 274:22618-22626(1999).
DR EMBL; AF17255; AAD48370.1; -.
KW Receptor.
FT NON_TER
SQ SEQUENCE 129 AA; 13990 MW; 7BE487F716CCDD48 CRC64;

Query Match
Best Local Similarity 83.3%; Score 5; DB 4; Length 129;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVD 5
Db 98 RKLVD 102

RESULT 14
Q98F36 PRELIMINARY; PRT; 148 AA.
AC Q98F36;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, last annotation update)
DE ACETYLPANSEFERASE.
GN MUR3958.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Ideasa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003003; BAB50731.1; -.
DR InterPro; IPR000182; Acetyltransf_GCN5.
DR Pfam; PF00583; Acetyltransf_1.
KW transferase; Complete proteome.
SQ SEQUENCE 148 AA; 17075 MW; A59FAEB203CEADF CRC64;

Query Match
Best Local Similarity 83.3%; Score 5; DB 16; Length 148;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVD 5
Db 130 RKLVD 134

RESULT 15
Q9AUJ1 PRELIMINARY; PRT; 157 AA.
AC Q9AUJ1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE MADS BOX PROTEIN NMADS1 (FRAGMENT).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]

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RP SEQUENCE FROM N.A.
RA Yuan Z., Qian X., Liu J., Liu J., Qian M., Yang J., Liu J.;
RT "Cloning and characterization of two cDNAs encoding rice MADS box
RT protein.";
RL Prog. Nat. Sci. 10:357-363(2000).
DR EMBL; AF095645; AAK26240.1; -.
DR HSSP; P11746; 1NMW.
DR InterPro; IPR002487; K-box.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TE; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PSS0066; MADS_BOX_2; 1.
FT NON_TER
SQ SEQUENCE 157 AA; 18145 MW; 05622210C95BAF32 CRC64;

Query Match
Best Local Similarity 83.3%; Score 5; DB 10; Length 157;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KLYDY 6
Db 46 KLYDY 50

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Search completed: November 8, 2002, 09:38:33
Job time : 27 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:21 ; Search time 4.66667 Seconds

(Without alignments)
49.782 Million cell updates/sec

Title: US-09-657-431-11

Perfect score: 34

Sequence: 1 RKLXDY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	34	100.0	810 1	PLMN_HUMAN
2	34	100.0	812 1	PLMN_MOUSE
3	32	94.1	295 1	YFEL_YEAST
4	32	94.1	439 1	GFO_ZYMO
5	31	91.2	190 1	RL5_METJA
6	31	91.2	434 1	ENO_STRPY
7	31	91.2	1113 1	ENO_STRPY
8	31	91.2	1161 1	Y140_MYCPN
9	31	91.2	1534 1	RPO2_FOMPV
10	31	91.2	1534 1	DNM1_ARATH
11	30	88.2	144 1	G10_XENLA
12	30	88.2	333 1	PLMN_CANFA
13	30	88.2	343 1	PLMN_SHEEP
14	30	88.2	426 1	YK96_AERPE
15	30	88.2	504 1	SIK1_YEAST
16	30	88.2	810 1	PLMN_ERIEU
17	30	88.2	810 1	PLMN_MCMU
18	30	88.2	959 1	K6P2_YEAST
19	30	88.2	4548 1	APOR_HUMAN
20	29	85.3	177 1	YAL6_SCHPO
21	29	85.3	305 1	DDU1_BACDH
22	29	85.3	405 1	DCDA_HELPJ
23	29	85.3	405 1	DCDA_HELPJ
24	29	85.3	488 1	EXON_HSV6U
25	29	85.3	488 1	EXON_HSV6Z
26	29	85.3	690 1	Y173_UREPA
27	29	85.3	822 1	DEXT_STRSL
28	29	85.3	974 1	CC15_YEAST
29	29	85.3	1202 1	RPM2_YEAST
30	28	82.4	90 1	MS2B_YEAST
31	28	82.4	90 1	MS2B_DROME
32	28	82.4	90 1	MS2B_DROME
33	28	82.4	90 1	MS2B_DROSI

34	28	82.4	187 1	DDP1_YEAST	Q99321	saccharomyc
35	28	82.4	205 1	ENGB_BUCAL	P57507	buchnera ap
36	28	82.4	327 1	VP35_FOPWY	Q91590	fovi1pox vir
37	28	82.4	413 1	YV40_CAEEL	O45435	caenorhabdi
38	28	82.4	443 1	ADA2_HUMAN	075478	homo sapien
39	28	82.4	505 1	VGIC_HSVMG	P10681	marek's dis
40	28	82.4	536 1	SCD2_SCHPO	P40996	schizosach
41	28	82.4	724 1	P85A_BOVIN	P23727	bos taurus
42	28	82.4	724 1	P85A_HUMAN	P27986	homo sapien
43	28	82.4	724 1	P85A_MOUSE	P26450	mus musculu
44	28	82.4	724 1	P85A_RAT	O63787	rattus norv
45	27	79.4	103 1	Y0BF_BACSU	P45922	bacillus su

ALIGNMENTS

RESULT 1	PLMN_HUMAN	STANDARD;	PRT;	810 AA.
ID	PLMN_HUMAN			
AC	P00747;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-MAR-1989 (Rel. 10, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].			
GN	PLG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=87162490; PubMed=3030813;			
RA	Forsgren M., Raden B., Israelsson M., Larsson K., Heden L.-O.;			
RT	"Molecular cloning and characterization of a full-length cDNA clone			
RT	for human plasminogen.";			
RL	FEBS Lett. 213:254-260(1987).			
RN	[3]			
RA	SEQUENCE OF 20-810.			
RT	Sottrop-Jensen L., Petersen T.E., Magnusson S.;			
RT	Submitted (JUL-1977) to the PIR data bank.			
RN	[4]			
RX	SEQUENCE OF 292-810 FROM N.A.			
RA	MEDLINE=85023311; PubMed=6148961;			
RT	Mallinowski D.P., Sadler J.E., Davie E.W.;			
RT	"Characterization of a complementary deoxyribonucleic acid coding for			
RL	human and bovine plasminogen.";			
RN	Biochemistry 23:4243-4250(1984).			
RN	[5]			
RA	SEQUENCE OF 20-100.			
RT	MEDLINE=75093329; PubMed=122932;			
RT	Wiman B., Wallen P.;			
RT	"Structural relationship between 'glutamic acid' and 'lysine' forms			
RT	of human plasminogen and their interaction with the NH2-terminal			
RT	activation peptide as studied by affinity chromatography.";			
RL	Eur. J. Biochem. 50:489-494(1975).			
RN	[6]			
RA	SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810.			
RT	Sottrop-Jensen L., Claess H., Zajdel M., Petersen T.E., Magnusson S.;			
RT	(In) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);			
RT	Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,			
RL	Raven Press, New York (1978).			
RN	[7]			
RA	SEQUENCE OF 483-604.			
RT	MEDLINE=76043692; PubMed=126863;			
RT	Wiman B., Wallen P.;			

- RT "Amino-acid sequence of the cyanogen-bromide fragment from human
RT plasminogen that forms the linkage between the plasmin chains.";
RL Eur. J. Biochem. 58:539-547(1975).
RN [8]
RX SEQUENCE OF 581-810.
RN MEDLINE=77225245; PubMed=142009;
RA Wilman B.;
RT "Primary structure of the B-chain of human plasmin.";
RL Eur. J. Biochem. 76:129-137(1977).
RN [9]
RP ACTIVE SITE.
RX MEDLINE=73149248; PubMed=4694729;
RA Robbins K.C., Bernabe P., Arzadon L., Summaria L.;
RT "The primary structure of human plasminogen. II. The histidine loop
RT of human plasmin: light (B) chain active center histidine sequence.";
RL J. Biol. Chem. 248:1631-1633(1973).
RN [10]
RP ACTIVE SITE.
RX MEDLINE=69234739; PubMed=4240117;
RA Groskopf W.R., Summaria L., Robbins K.C.;
RT "Studies on the active center of human plasmin. Partial amino acid
RT sequence of a peptide containing the active center serine residue.";
RL J. Biol. Chem. 244:3590-3597(1969).
RN [11]
RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RX MEDLINE=82213905; PubMed=6919539;
RA Trexler M., Valli Z., Pathy L.;
RT "Structure of the omega-aminocarboxylic acid-binding sites of human
RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
RT binding of ligand by kringle 4.";
RL J. Biol. Chem. 257:7401-7406(1982).
RN [12]
RP FLBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RX MEDLINE=85054794; PubMed=6094526;
RA Valli Z., Pathy L.;
RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
RT are essential for fibrin affinity of the kringle 1 domain.";
RL J. Biol. Chem. 259:13690-13694(1984).
RN [13]
RP PHOSPHORYLATION SITE SER-597.
RX MEDLINE=97345939; PubMed=9201958;
RA Wang H., Protor M., Brethauer R.K., Castellino F.J.;
RT "Serine-578 is a major phosphorylation locus in human plasma
RT plasminogen.";
RL Biochemistry 36:8100-8106(1997).
RN [14]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=88185329; PubMed=3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
RT Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63(1988).
RN [15]
RP CARBOHYDRATE-LINKAGE SITE 268.
RX MEDLINE=97207306; PubMed=9054441;
RA Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,
RT Pizzo S.V.;
RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
RT human plasminogen 2.";
RL J. Biol. Chem. 272:7408-7411(1997).
RN [16]
RP CHARACTERIZATION OF ANGIOSTATIN AND PARTIAL SEQUENCE.
RX MEDLINE=95042728; PubMed=7525077;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RT Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma.";
RL Cell 79:315-328(1994).
RN [17]
RP CHARACTERIZATION OF ANGIOSTATIN.
RX MEDLINE=97238710; PubMed=9102221;
RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
RA Lapevich R., Nacy C.A.;
RT "A recombinant human angiostatin protein inhibits experimental primary
RT and metastatic cancer.";
RL Cancer Res. 57:1329-1334(1997).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RX MEDLINE=92031502; PubMed=1657148;
RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
RT "Crystal and molecular structure of human plasminogen kringle 4
RT refined at 1.9-A resolution.";
RL Biochemistry 30:10576-10588(1991).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RX MEDLINE=92031503; PubMed=1657149;
RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of
RT human plasminogen kringle 4.";
RL Biochemistry 30:10589-10594(1991).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RA Stec B., Yamano A., Whitlow M., Teeter M.M.;
RL Submitted (JUN-1995) to the PDB data bank.
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
RX MEDLINE=96180681; PubMed=8611560;
RA Mathews I.I., Vanderhoff-Hanaver P., Castellino F.J., Tulinsky A.;
RT "Crystal structures of the recombinant kringle 1 domain of human
RT plasminogen in complexes with the ligands epsilon-aminocaproic acid
RT and trans-4-(aminomethyl)cyclohexane-1-carboxylic acid.";
RL Biochemistry 35:2567-2576(1996).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
RX MEDLINE=98198034; PubMed=9521645;
RA Chang Y., Mochalkin I., Mccance S.G., Cheng B., Tulinsky A.,
RA Castellino F.J.;
RT "Structure and ligand binding determinants of the recombinant kringle
RT 5 domain of human plasminogen.";
RL Biochemistry 37:3258-3271(1998).
RN [23]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237157; PubMed=8181475;
RA Rejzante M.R., Llinas M.;
RT "1H-NMR assignments and secondary structure of human plasminogen
RT kringle 1.";
RL Eur. J. Biochem. 221:927-937(1994).
RN [24]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237158; PubMed=8181476;
RA Rejzante M.R., Llinas M.;
RT "Solution structure of the epsilon-aminohexanoic acid complex of
RT human plasminogen kringle 1.";
RL Eur. J. Biochem. 221:939-949(1994).
RN [25]
RP STRUCTURE BY NMR OF 183-354.
RX MEDLINE=96194156; PubMed=8652577;
RA Soehnel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
RA Rickli E.E.;
RT "Recombinant gene expression and 1H NMR characteristics of the
RT kringle (2 + 3) supermodule: spectroscopic/functional individuality
RT of plasminogen kringle domains.";
RL Biochemistry 35:2357-2364(1996).
RN [26]
RP STRUCTURE BY NMR OF 374-461.
RX MEDLINE=90219023; PubMed=2157850;
RA Atkinson R.A., Williams R.J.P.;
RT "Solution structure of the kringle 4 domain from human plasminogen by
RT 1H nuclear magnetic resonance spectroscopy and distance geometry.";
RL J. Mol. Biol. 212:541-552(1990).
RN [27]
RP VARIANTS PHE-374 AND THR-620.
RX MEDLINE=91095410; PubMed=1986355;
RA Ichinose A., Espling E.S., Takamatsu J., Saito H., Shimoyozu K.,

Query Match 100.0%; Score 34; DB 1; Length 810;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLXDY 6
 |||||
 DB 549 RKLXDY 554

RESULT 2
 PLMN_MOUSE STANDARD; PRT: 812 AA.
 ID PLMN_MOUSE STANDARD; PRT: 812 AA.
 AC P20918:
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
 GN PLG.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=91184812; PubMed=2081600;
 RX Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
 RA "Characterization of the cDNA coding for mouse plasminogen and
 RT localization of the gene to mouse chromosome 17.";
 RL Genomics 8:49-61(1990).
 RN [2]
 RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
 RX MEDLINE=95042728; PubMed=7525077;
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 RA Moses W., Lane W.S., Cao Y., Sage E.H., Folkman J.;
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
 RT suppression of metastases by a Lewis lung carcinoma.";
 RL Cell 79:315-328(1994).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE URKININASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
 CC NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
 CC METASTATIC TUMORS IN VIVO.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
 CC INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD
 CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
 CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
 CC -1- This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J04766; AAA50168.1; -
 DR PIR: A38514; A38514.
 DR HSSP: P00747; 1PMK.

DR MEROPS; S01.233; -
 DR MGD; MG1:97620; PLG.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR01254; Trypsin.
 DR Pfam: PF00051; Kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0018; KRINGLE.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS0070; KRINGLE_2; 5.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 DR Hydrolase: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 812 PLASMINOGEN.
 FT CHAIN 20 581 PLASMIN HEAVY CHAIN A.
 FT PEPTIDE 20 97 ACTIVATION PEPTIDE.
 FT CHAIN 98 581 PLASMIN SHORT FORM OF CHAIN A.
 FT CHAIN 98 7436 ANGIOSTATIN.
 FT CHAIN 582 812 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 103 181 KRINGLE 1.
 FT DOMAIN 184 262 KRINGLE 2.
 FT DOMAIN 275 352 KRINGLE 3.
 FT DOMAIN 377 454 KRINGLE 4.
 FT DOMAIN 481 560 KRINGLE 5.
 FT DOMAIN 582 812 SERINE PROTEASE.
 FT ACT_SITE 624 624 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 667 667 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 762 762 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 49 73 BY SIMILARITY.
 FT DISULFID 53 61 BY SIMILARITY.
 FT DISULFID 103 181 BY SIMILARITY.
 FT DISULFID 124 164 BY SIMILARITY.
 FT DISULFID 152 176 BY SIMILARITY.
 FT DISULFID 185 262 BY SIMILARITY.
 FT DISULFID 188 316 BY SIMILARITY.
 FT DISULFID 206 245 BY SIMILARITY.
 FT DISULFID 234 257 BY SIMILARITY.
 FT DISULFID 275 352 BY SIMILARITY.
 FT DISULFID 296 335 BY SIMILARITY.
 FT DISULFID 324 347 BY SIMILARITY.
 FT DISULFID 377 454 BY SIMILARITY.
 FT DISULFID 398 437 BY SIMILARITY.
 FT DISULFID 426 449 BY SIMILARITY.
 FT DISULFID 481 560 BY SIMILARITY.
 FT DISULFID 502 543 BY SIMILARITY.
 FT DISULFID 531 555 BY SIMILARITY.
 FT DISULFID 568 687 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 578 586 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 609 625 BY SIMILARITY.
 FT DISULFID 701 768 BY SIMILARITY.
 FT DISULFID 731 747 BY SIMILARITY.
 FT DISULFID 758 786 BY SIMILARITY.
 FT SEQUENCE 812 AA; 90846 MW; D34A74A4FC2256F8 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 812;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKLXDY 6
 |||||
 DB 549 RKLXDY 554

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RESULT 3
YFLL YEAST
ID YFLL YEAST STANDARD: PRT: 295 AA.
AC P43613;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 34.2 kDa protein in SAP15-YMR31 intergenic region
DE precursor.
GN YFRO41C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Seda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae."
RL Nat. Genet. 10:261-268(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=96287652; PubMed=8686379;
RA Eki T., Naitou M., Hagiwara H., Ozawa M., Sasanuma S.-I.,
RA Sasanuma M., Tsuchiya Y., Shibata T., Hanaoka F., Murakami Y.;
RT "Analysis of a 36.2 kb DNA sequence including the right telomere of
RT chromosome VI from Saccharomyces cerevisiae."
RL Yeast 12:149-167(1996).
RN [3]
RP -1 SIMILARITY: CONTAINS 1 J DOMAIN.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D50617; BAA09280.1; -
CC DR EMBL: D44597; BAA08007.1; -
CC DR HSSP: P25685; 1HDJ.
CC DR SGD: S0001937; YFRO41C.
CC DR InterPro: IPR001623; DnaJ_N.
CC DR Pfam: PF00226; DnaJ_1.
CC DR SMART: SM00271; DnaJ_1.
CC DR PROSITE: PS00636; DnaJ_1; 1.
CC DR PROSITE: PS50076; DnaJ_2; 1.
CC DR Hypothetical protein; Chapterone; Signal.
CC FT SIGNAL 1 20 POTENTIAL.
CC FT CHAIN 21 295 HYPOTHETICAL PROTEIN YFRO41C.
CC FT DOMAIN 42 110 J-DOMAIN.
CC SQ SEQUENCE 295 AA; 34191 MW; 4541BF6C35DB8AC CRC64;

Query Match 94.1%; Score 32; DB 1; Length 295;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
Db 101 RKLYDY 106

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DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glucose--fructose oxidoreductase precursor (BC 1.1.99.28) (GFOR).
GN GFO.
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
OC Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 53-87.
RC STRAIN=ATCC 29191 / ZM6;
RX MEDLINE=92165717; PubMed=1537789;
RA Kanagasundaram V., Scopes R.K.;
RT "Cloning, sequence analysis, and expression of the structural gene
RT encoding glucose-fructose oxidoreductase from Zymomonas mobilis."
RL J. Bacteriol. 174:1439-1447(1992).
RN [2]
RP SEQUENCE OF 1-71 FROM N.A., AND SEQUENCE OF 2-16 AND 53-71.
RC STRAIN=ATCC 29191 / ZM6, AND ATCC 31821 / ZM4 / CP4;
RX MEDLINE=93231476; PubMed=8472911;
RA Loos H., Sahm H., Sprenger G.A.;
RT "Glucose-fructose oxidoreductase, a periplasmic enzyme of Zymomonas
RT mobilis, is active in its precursor form."
RL FEWS Microbiol. Lett. 107:293-298(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97148336; PubMed=8994968;
RA Kingston R.L., Scopes R.K., Baker E.N.;
RT "The structure of glucose-fructose oxidoreductase from Zymomonas
RT mobilis: an osmoprotective periplasmic enzyme containing non-
RT dissociable NADP."
RL Structure 4:1413-1428(1996).
RN [4]
RP -1 CATALYTIC ACTIVITY: D-glucose + D-fructose = D-gluculonolactone + D-
RP glucitol.
CC -----
CC -1 COFACTOR: CONTAINS ONE TIGHTLY-BOUND NADP(H) MOLECULE PER SUBUNIT.
CC -1 PATHWAY: SORBITOL-GLUCONATE PATHWAY.
CC -1 SUBUNIT: HOMOTETRAMER.
CC -1 SUBCELLULAR LOCATION: Periplasmic.
CC -1 SIMILARITY: BELONGS TO THE GFO/IDH/MOCA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M97379; AAA27690.1; -
CC DR EMBL: X73088; CAA51534.1; -
CC DR PDB: 1OFG; 21-APR-97.
CC DR InterPro: IPR000683; GFO_IDH_MOCA.
CC DR InterPro: IPR004104; GFO_IDH_MOCA_C.
CC DR Pfam: PF01408; GFO_IDH_MOCA_1.
CC DR Pfam: PF02894; GFO_IDH_MOCA_C; 1.
CC DR Oxidoreductase; NADP; Signal; Periplasmic; 3D-structure.
CC FT SIGNAL 1 52
CC FT CHAIN 53 439 GLUCOSE--FRUCTOSE OXIDOREDUCTASE.
CC FT CONFLICT 61 61 L->O (TN REF. 2; AA SEQUENCE).
CC FT CONFLICT 61 61
CC SQ SEQUENCE 439 AA; 47801 MW; C1E4A19F534267A CRC64;

Query Match 94.1%; Score 32; DB 1; Length 439;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
Db 133 RKLYDY 138

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RESULT 4
GFO_ZYMOO
ID GFO_ZYMOO STANDARD: PRT: 439 AA.
AC Q07982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

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RESULT 5
RL5_META
ID RL5_META STANDARD: PRT: 190 AA.
AC P54040;

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DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L5P.
GN RPL5P OR M0469
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
CC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=9633799; PubMed=688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cofon M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Kleen H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii".
RL Science 273:1056-1073(1996).
CC -1- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U67497; AAB98458.1; -.
DR InterPro: IPR002132; Ribosomal_L5.
DR Pfam: PF00281; Ribosomal_L5_C; 1.
DR ProDom: PD001076; Ribosomal_L5; 1.
DR PROSITE: PS00358; RIBOSOMAL_L5; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 190 AA; 22169 MW; BD0536973C3A533 CRC64;

Query Match 91.2%; Score 31; DB 1; Length 190;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVDY 6
Db 95 KKLVDY 100

RESULT 6
ENO_STRIT STANDARD; PRT; 434 AA.
AC Q9XDS7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
DE glycerate hydro-lyase).
GN ENO.
OS Streptococcus intermedius.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
CC Streptococcus.
OX NCBI_TaxID=1338;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 27335;
RA Sato S.;
RT "Streptococcus intermedius enolase gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

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CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H2O.
CC -1- COPACITOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----
DR EMBL: AB029313; BAA81815.1; -.
DR HSSP: P00924; ENL.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium.
FT ACT_SITE 155 155
FT METAL 242 242
FT METAL 291 291
FT METAL 318 318
SQ SEQUENCE 434 AA; 47015 MW; AA0D39DA832BA4F3B CRC64;

Query Match 91.2%; Score 31; DB 1; Length 434;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVDY 6
Db 253 RKLVDY 258

RESULT 7
ENO_STRPY STANDARD; PRT; 434 AA.
AC P82479;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
DE glycerate hydro-lyase).
GN ENO OR SPY0731.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
CC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.-J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Szentei S., Suvorov A.N., Kerton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN [2]
RP PARTIAL SEQUENCE, AND MASS SPECTROMETRY.
RC STRAIN-JRS4 / Serotype M6;
RA Hogan D.A., Du P., Stevenson T.I., Whittom M., Kilby G.W., Rogers J.,
RA Vanbogaellen R.A.;
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT proteins.";
RL Submitted (MAY-2000) to the SWISS-PROT data bank.
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +

```

```

CC H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----
DR EMBL: AE006524; AAK33680.1; -.
DR HSSP: P00924; IONE.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 4.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
DR Lyase: Glycolysis; Magnesium; Complete proteome.
KW INIT_MET 0 0
FT ACT_SITE 154 154 BY SIMILARITY.
FT METAL 242 242 MAGNESIUM (BY SIMILARITY).
FT METAL 291 291 MAGNESIUM (BY SIMILARITY).
FT METAL 318 318 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 434 AA; 47225 MW; 34FD4FC4D7D25B44 CRC64;

Query Match
Best Local Similarity 83.3%; Pred. NO. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
DB 253 RKVYDY 258

RESULT 8
Y140_MYCPN STANDARD; PRT; 1113 AA.
ID Y140_MYCPN
AC P75033;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical ATP-binding protein M6140 Homolog (E07_orf113).
GN MPN153 OR MP001.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelfreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA Hermann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SIMILARITY: BELONGS TO THE DNA2/NAM7 HELICASE FAMILY.
CC -----
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CC -----
DR EMBL: AE000001; AAB95649.1; -.

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KW Hypothetical protein; ATP-binding; Helicase; Complete proteome.
FT NP_BIND 313 320 ATP (POTENTIAL).
SQ SEQUENCE 1113 AA; 130333 MW; 48A3337EB0E81A40 CRC64;

Query Match
Best Local Similarity 83.3%; Score 31; DB 1; Length 1113;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
DB 693 RKVYDY 698

RESULT 9
RP02_F0MPV STANDARD; PRT; 1161 AA.
ID RP02_F0MPV
AC Q95044;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase 132 kDa polypeptide (EC 2.7.7.6).
GN RP0132 OR F0V189.
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2019820; PubMed=10729156;
RA Alfonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus."
RL J. Virol. 74:3815-3831(2000).
CC -1- SUBUNIT: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -1- SUBUNIT: THIS ENZYME CONSISTS OF AT LEAST EIGHT SUBUNITS.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
CC -----
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CC -----
DR EMBL: AF198100; AAF44533.1; -.
DR InterPro: IPR001572; RNA_POL_B.
DR Pfam: PF00562; RNA_POL_B; 1.
DR PROSITE: PS01166; RNA_POL_BETA; 1.
KW Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
KW Zinc-finger.
FT ZN_FING 1079 1098 C4-TYPE (POTENTIAL).
SQ SEQUENCE 1161 AA; 133468 MW; 334C2FC5D65384F CRC64;

Query Match
Best Local Similarity 83.3%; Score 31; DB 1; Length 1161;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
DB 647 KKLVDY 652

RESULT 10
DNM1_ARATH STANDARD; PRT; 1534 AA.
ID DNM1_ARATH
AC P34861;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)

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DE DNA (cytosine-5)-methyltransferase Ath1 (EC 2.1.1.37) (DNA
DE methyltransferase Ath1) (DNA Metase Ath1) (M.Ath1).
GN ARHM OR AT5G49160 OR K21P3.3.
OS Arabidopsis thaliana (Mouse-ear cress).
CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA:
RX MEDLINE=93281384; PubMed=8389441;
RA Finnegan E.J., Dennis E.S.;
RT "Isolation and identification by sequence homology of a putative
RT cytosine methyltransferase from Arabidopsis thaliana.";
RL Nucleic Acids Res. 21:2383-2388(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA:
RX MEDLINE=99156233; PubMed=10048488;
RA Asamizu E., Sato S., Kaneo T., Nakamura Y., Kotani H., Miyaajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
RT Sequence features of the regions of 1,081,958 bp covered by seventeen
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:379-381(1998).
CC -1- FUNCTION: METHYLATES CG RESIDUES.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA = S-adenosyl-L-
CC homocysteine + DNA containing 5-methylcytosine.
CC -1- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
CC -1- SIMILARITY: CONTAINS 2 BAH DOMAINS.
CC -----
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CC -----
CC
CC EMBL: L10692; AAA32829.1; -.
CC DR EMBL; AB016872; BAB10334.1; -.
CC DR REBASE: 2839; M.Ath1.
CC DR InterPro: IPR001025; BAH.
CC DR InterPro: IPR001525; C5_DNA_meth.
CC DR Pfam: PF01426; BAH; 2.
CC DR Pfam: PF00145; DNA_methylase; 3.
CC DR PRINTS: PR00105; C5METTRFRASE.
CC DR SMART: SM00439; BAH; 2.
CC DR PROSITE: PS00095; C5_MTASE_1; 1.
CC DR PROSITE: PS00095; C5_MTASE_2; 1.
CC DR Transferrase: Methyltransferase; DNA-binding.
CC KW TRANSFERASE; Methyltransferase; DNA-binding.
CC FT ACT_SITE 1198 1198 BY SIMILARITY.
CC SQ SEQUENCE 1534 AA; 172430 MW; 23FC944AA7074C5A CRC64;
Query Match 91.2%; Score 31; DB 1; Length 1534;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 RKLYDY 6
ID 111111
Db 172 RKVYDY 177

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89306617; PubMed=2568313;
RA McGrew L.L., Dworkin-Rastl E., Dworkin M.B., Richter J.D.;
RT "Poly(A) elongation during Xenopus oocyte maturation is required for
RT translational recruitment and is mediated by a short sequence
RT element.";
RL Genes Dev. 3:803-815(1989).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- DEVELOPMENTAL STAGE: OOCYTE MATURATION IS ACCOMPANIED BY THE
CC RECRUITMENT OF SPECIFIC MATERNAL MRNAS INTO POLYSOMES. G10 IS AN
CC EXAMPLE OF A PROTEIN WHICH IS TRANSLATED AT THAT TIME.
CC -1- SIMILARITY: BELONGS TO THE G10 FAMILY.
CC -----
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CC -----
CC
CC EMBL: X15243; CAA33321.1; -.
CC DR PTR; S05955; S05955.
CC DR InterPro: IPR001748; G10.
CC DR Pfam: PF01125; G10; 1.
CC DR PRINTS: PR00322; G10.
CC DR PRODOM: PD009460; G10; 1.
CC DR PROSITE: PS00997; G10_1; 1.
CC DR PROSITE: PS00998; G10_2; 1.
CC DR Developmental protein; Nuclear protein; Zinc-finger
CC KW DOMAIN 2 10 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT ZN_FING 101 119 POTENTIAL.
CC SQ SEQUENCE 144 AA; 17040 MW; D2AVD3D4E398B696 CRC64;
Query Match 88.2%; Score 30; DB 1; Length 144;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 RKLYDY 6
ID 111111
Db 72 RKVYDY 77

RESULT 12
ID PLMN_CANFA STANDARD; PTR; 333 AA.
AC P80009;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Plasmalogen (EC 3.4.21.7) (Fragment).
GN PLG.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE-Plasma;
RX MEDLINE=90175323; PubMed=2626424;
RA Schaller J., Straub C., Kaempfer U., Rickli E.E.;
RT "Complete amino acid sequence of canine miniplasminogen.";
RL Protein Seq. Data Anal. 2:445-450(1989).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION. IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UKONINASE-TYPE PLASMINOGEN

CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. ACTIVATED WITH UROKINASE AND HIGH CONCENTRATIONS OF
 CC STREPTOKINASE.
 CC MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS AT LEAST 1 KRINGLE DOMAIN.
 CC HSP; P00747; 5HPG.
 CC MEROPS: S01.233; -.
 CC InterPro: IPR000001; Kringle.
 CC InterPro: IPR001254; Trypsin.
 CC Pfam: PF00051; kringle; 1.
 CC Pfam: PF00089; trypsin; 1.
 CC SMART: SM00130; KR; 1.
 CC SMART: SM00020; TRYP-SPC; 1.
 CC PROSITE: PS00021; KRINGLE_1; 1.
 CC PROSITE: PS00070; KRINGLE_2; 1.
 CC PROSITE: PS00240; TRYPsin_DOM; 1.
 CC PROSITE: PS00134; TRYPsin_HIS; 1.
 CC PROSITE: PS00135; TRYPsin_SER; 1.
 CC PROSITE: PS00135; TRYPsin_SER; 1.
 CC Hydrolase: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 CC Tissue remodeling; Blood coagulation; Kringle; Zymogen.
 CC NON_TER 1
 CC CHAIN <1 103 PLASMIN HEAVY CHAIN A.
 CC CHAIN 104 333 PLASMIN LIGHT CHAIN B.
 CC DOMAIN 4 83 KRINGLE 5.
 CC DOMAIN 104 333 SERINE PROTEASE.
 CC DISULFID 4 83 BY SIMILARITY.
 CC DISULFID 25 66 BY SIMILARITY.
 CC DISULFID 54 78 BY SIMILARITY.
 CC DISULFID 90 208 INTERCHAIN (BY SIMILARITY).
 CC DISULFID 100 108 INTERCHAIN (BY SIMILARITY).
 CC DISULFID 130 146 BY SIMILARITY.
 CC DISULFID 222 289 BY SIMILARITY.
 CC DISULFID 252 268 BY SIMILARITY.
 CC DISULFID 279 307 BY SIMILARITY.
 CC ACT_SITE 145 145 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT_SITE 188 188 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT_SITE 283 283 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC SITE 152 152 STREPTOKINASE-BINDING SITE (PROBABLE).
 CC SITE 186 186 STREPTOKINASE-BINDING SITE (PROBABLE).
 CC SITE 264 264 STREPTOKINASE-BINDING SITE (PROBABLE).
 CC SITE 277 277 SITE OF SUBSTRATE SPECIFICITY
 CC SITE (BY SIMILARITY).
 CC SEQUENCE 333 AA; 36678 MW; C6C0271B6C6ACBD4 CRC64;
 SQ

Query Match 88.2%; Score 30; DB 1; Length 333;
 Best Local Similarity 83.3%; Pred. No. 44;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYDY 6
 |||:|
 Db 72 RKLFDY 77

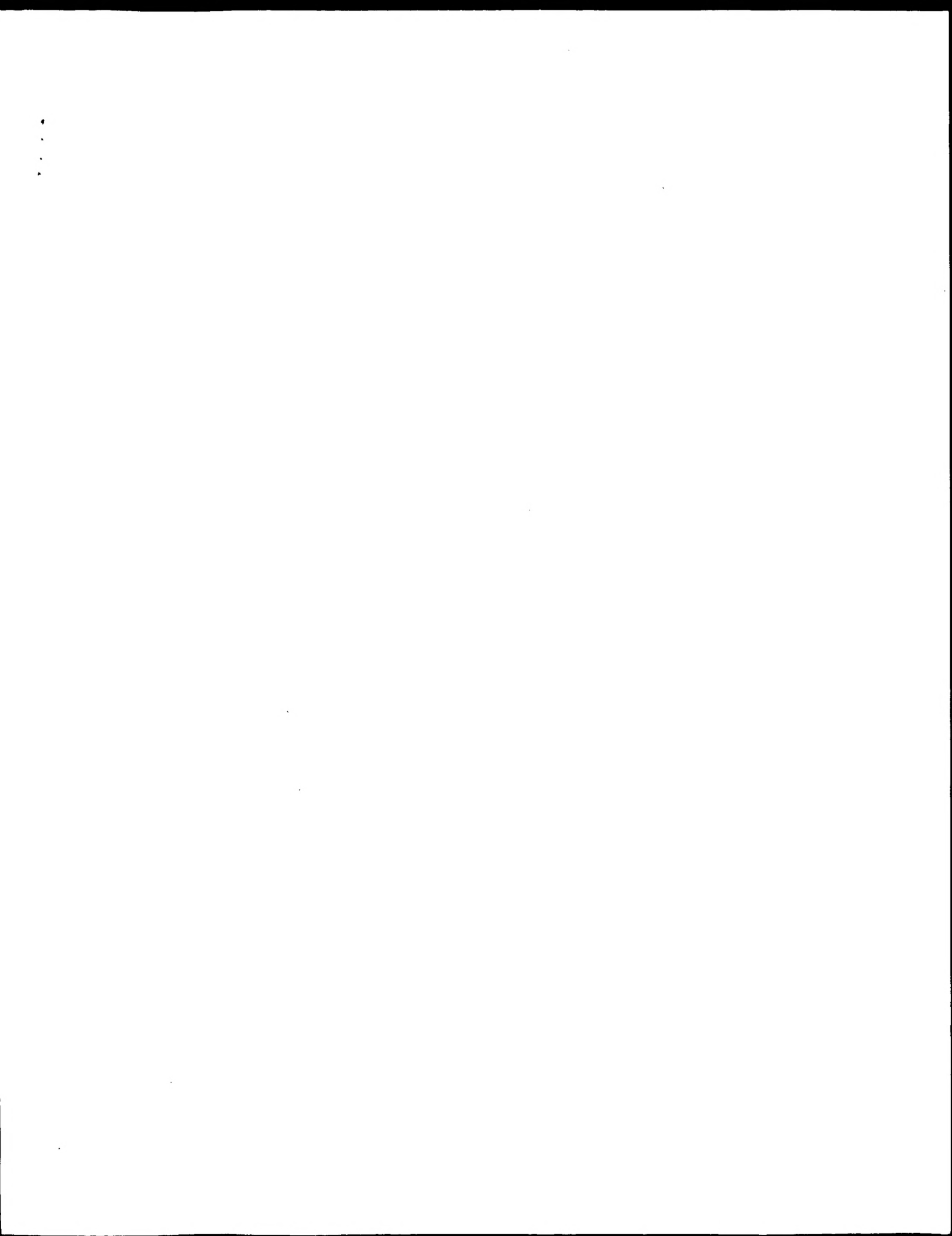
RESULT 13
 PLMN_SHEEP
 ID PLMN_SHEEP STANDARD; PRT; 343 AA.
 AC P81286; 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasmalogen (EC 3.4.21.7) (Fragment).
 GN PLG
 OS Ovis aries (Sheep).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=9314995; PubMed=1492092;
 RA Schaller J., Straub C., Kamper U., Rickl E.E.
 RT "Complete amino acid sequence of ovine miniplasminogen.";
 RL Protein Seq. Data Anal. 5:21-25(1992).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS AT LEAST 2 KRINGLE DOMAINS.
 CC HSP; P00747; 5HPG.
 CC MEROPS: S01.233; -.
 CC InterPro: IPR000001; Kringle.
 CC InterPro: IPR001254; Trypsin.
 CC Pfam: PF00051; kringle; 1.
 CC Pfam: PF00089; trypsin; 1.
 CC SMART: SM00130; KR; 1.
 CC SMART: SM00020; TRYP-SPC; 1.
 CC PROSITE: PS00021; KRINGLE_1; 1.
 CC PROSITE: PS00070; KRINGLE_2; 1.
 CC PROSITE: PS00240; TRYPsin_DOM; 1.
 CC PROSITE: PS00134; TRYPsin_HIS; 1.
 CC PROSITE: PS00135; TRYPsin_SER; 1.
 CC Hydrolase: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 CC Tissue remodeling; Blood coagulation; Kringle; Zymogen.
 CC NON_TER 1
 CC CHAIN <1 140 HEAVY CHAIN A.
 CC CHAIN 141 343 LIGHT CHAIN A.
 CC DOMAIN <1 17 KRINGLE 4.
 CC DOMAIN 41 120 KRINGLE 5.
 CC DOMAIN 114 341 SERINE PROTEASE.
 CC ACT_SITE 181 181 CHARGE RELAY SYSTEM.
 CC ACT_SITE 224 224 CHARGE RELAY SYSTEM.
 CC ACT_SITE 319 319 CHARGE RELAY SYSTEM.
 CC ACT_SITE 343 343 CHARGE RELAY SYSTEM.
 CC SEQUENCE 343 AA; 37662 MW; 8DF6EBA92D596EED0 CRC64;
 SQ

Query Match 88.2%; Score 30; DB 1; Length 343;
 Best Local Similarity 83.3%; Pred. No. 45;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYDY 6
 |||:|
 Db 83 RKLFDY 88

RESULT 14
 YK96_AERPE
 ID YK96_AERPE STANDARD; PRT; 426 AA.
 AC Q9YA42; 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein APE2096.
 GN APE2096.
 OS Aeropyrum pernix.
 CC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
 CC Aeropyrum.
 CC NCBI_TaxID=56636;
 RN [1]





GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:22 : Search time 14.3333 Seconds
(without alignments)
72.416 Million cell updates/sec

Title: US-09-657-431-11

Perfect score: 34

Sequence: 1 RKLXDY 6

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.potent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	334	6	046507 papio hamad
2	34	100.0	810	4	015146 homo sapien
3	34	100.0	812	11	09ROW3 ratus norv
4	34	100.0	812	11	091WJ5 mus musculu
5	32	94.1	73	12	007273 turkey rhin
6	32	94.1	254	16	09PMJ3 campylobact
7	32	94.1	404	16	09KVG1 campylobact
8	32	94.1	433	2	09KVG1 vibrio chol
9	31	91.2	274	5	p91014 caenorhabdi
10	31	91.2	388	9	038198 xanthomonas
11	31	91.2	409	16	099GCI staphylococ
12	31	91.2	417	2	045037 borrelia bu
13	31	91.2	417	16	050899 borrelia bu
14	31	91.2	434	2	0935W7 streptococ
15	31	91.2	434	16	0970S2 streptococ
16	31	91.2	454	10	09ZRW0 cicer arlet

17	31	91.2	499	10	09LTV0	09LTV0 arabidopsis
18	31	91.2	522	10	09SGT7	09SGT7 arabidopsis
19	31	91.2	584	5	09UDM8	09UDM8 plasmodium
20	31	91.2	633	5	097305	097305 plasmodium
21	31	91.2	1165	12	098839	098839 moliuscum c
22	31	91.2	1404	10	09T011	09T011 arabidopsis
23	31	91.2	1517	10	09SEG3	09SEG3 arabidopsis
24	31	91.2	1519	10	023273	023273 arabidopsis
25	30	88.2	144	5	097454	097454 drosophila
26	30	88.2	160	17	097CJ1	097CJ1 thermoplas
27	30	88.2	292	16	0970J3	0970J3 streptococ
28	30	88.2	294	16	099ZFE	099ZFE streptococ
29	30	88.2	319	16	097DR3	097DR3 clostridium
30	30	88.2	320	5	018887	018887 caenorhabdi
31	30	88.2	405	9	064073	064073 bacterioph
32	30	88.2	405	16	031948	031948 bacillus su
33	30	88.2	474	17	028424	028424 archaeoglob
34	30	88.2	502	16	09P0W1	09P0W1 ureaplasma
35	30	88.2	647	5	044560	044560 caenorhabdi
36	30	88.2	722	5	09V5F2	09V5F2 drosophila
37	30	88.2	732	2	09L281	09L281 streptomyc
38	30	88.2	1187	10	09ZV43	09ZV43 arabidopsis
39	30	88.2	1436	3	007527	007527 saccharomyc
40	29	85.3	73	12	090089	090089 turkey rhin
41	29	85.3	104	16	09PMK4	09PMK4 campylobact
42	29	85.3	146	11	092403	092403 mus musculu
43	29	85.3	148	16	098F36	098F36 rhizobium l
44	29	85.3	157	10	09A0J1	09A0J1 oryza sativ
45	29	85.3	170	2	09KX31	09KX31 streptococ

ALIGNMENTS

RESULT 1
ID 046507 PRELIMINARY; PRT; 334 AA.
AC 046507;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PLASMINOGEN (FRAGMENT).
GN BABPEPSG.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Cox L.A., Jett C., Hixson J.E.;
RT "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice Site Mutation is Associated with Deletion of a Single Exon in a Null Allele."
RT Allele."
RL Submitted (0CT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
CC EMBL; AF029692; AAB97887.1; -.
CC HESP; AF00747; 5HPG.
CC MEROPS; S01.233; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Trypsin.
DR Pfam; PF00051; kringle.1.
DR Pfam; PF00089; trypsin.1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR SMART; SM00130; KR.1.
DR SMART; SM00020; TRYP_SPE; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease.
 FT NON_TER
 SQ SEQUENCE 334 AA; 36791 MW; C7DC06F03B965286 CRC64;

Query Match 100.0%; Score 34; DB 6; Length 334;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
 |||||
 Db 73 RKLYDY 78

RESULT 2
 ID 015146 PRELIMINARY; PRT; 810 AA.

AC 015146; (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE PLASMINOGEN PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
 RA Mitchell D., Robinson J.H.;
 RT "Expression of recombinant human plasminogen and aglycoplasminogen in
 RT HeLa cells."
 RL Fibrinolysis 0:0-0(1991).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.

DR EMBL; M74220; AAA36451.1; -.
 DR HSSP; P00747; 2PK4.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00473; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS50070; KRINGLE_2; 5.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 810 PLASMINOGEN.
 SQ SEQUENCE 810 AA; 90555 MW; B05C7D4BD0D020B3C CRC64;

Query Match 100.0%; Score 34; DB 4; Length 810;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
 |||||
 Db 549 RKLYDY 554

RESULT 3
 Q9ROW3

ID Q9ROW3 PRELIMINARY; PRT; 812 AA.
 AC Q9ROW3;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE PLASMINOGEN PROTEIN PRECURSOR (BC 3.4.21.7).
 GN PLASMINOGEN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Bangert K., Johnsen A.H., Thorsen S.;
 RT "Rat plasminogen: cDNA and gene structure."
 RL submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE-91250378; PubMed-1645711;
 RA Kanakas J.J., Makker S.P.;
 RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
 RT receptor site for plasminogen."
 RL J. Biol. Chem. 266:10825-10829(1991).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.

DR EMBL; AJ242649; CAB46014.1; -.
 DR HSSP; P00747; 1PKK.
 DR MEROPS; S01.233; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001400; SOMATOTROPIN.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS50070; KRINGLE_2; 5.
 DR PROSITE; PS00336; SOMATOTROPIN_2; UNKNOWN_1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 812 PLASMINOGEN.
 SQ SEQUENCE 812 AA; 90535 MW; 8C703C51410EBC9E CRC64;

Query Match 100.0%; Score 34; DB 11; Length 812;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
 |||||
 Db 549 RKLYDY 554

RESULT 4
 Q91WJ5 PRELIMINARY; PRT; 812 AA.

ID Q91WJ5
 AC Q91WJ5;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE PLASMINOGEN.
 OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC014773; AAL14773.1; -;
 SQ SEQUENCE 812 AA; 90781 MW; 24173260E6A2FFD2 CRC64;

Query Match 100.0%; Score 34; DB 11; Length 812;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYDY 6
 |||||
 Db 549 RKLYDY 554

RESULT 5
 ID 007273 PRELIMINARY; PRT; 73 AA.
 AC 007273;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-FEB-1997 (TREMblrel. 02, Last annotation update)
 DE HYPOTHEICAL 8.5 KDA PROTEIN IN 22K 3'REGION.
 OS Turkey rhinotracheitis virus (TRRV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Metapneumovirus.
 ON NCBI_TaxID=11264;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UK/3BV/85;
 RA Yu Q., Davis P.J., Brown T.D.K., Cavanagh D.;
 RL J. Gen. Virol. 73:1355-1363(1993).
 DR EMBL: X63408; CAA45005.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 73 AA; 8488 MW; D6E09B8DC40EC4F CRC64;

Query Match 94.1%; Score 32; DB 12; Length 73;
 Best Local Similarity 83.3%; Pred. No. 13;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYDY 6
 |||||
 Db 25 RKLYDY 30

RESULT 6
 ID 09PMJ3 PRELIMINARY; PRT; 254 AA.
 AC 09PMJ3;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE HYPOTHEICAL PROTEIN CJI467.
 GN CJI467.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 OC Campylobacter.
 ON NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCTC 11168;
 MEDLINE=20150912; PubMed=10688204;
 RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
 RA Tagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
 RA Whitehead S., Barrell B.G.;
 *The genome sequence of the food-borne pathogen Campylobacter jejuni

RT reveals hypervariable sequences."
 RL Nature 403:665-668(2000).
 DR EMBL: AL139078; CAB73890.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 254 AA; 30201 MW; 15712EC3A70AD3E1 CRC64;

Query Match 94.1%; Score 32; DB 16; Length 254;
 Best Local Similarity 83.3%; Pred. No. 48;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYDY 6
 |||||
 Db 210 RKLYDY 215

RESULT 7
 ID 09KVG1 PRELIMINARY; PRT; 404 AA.
 AC 09KVG1;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE TRANSPOSASE, PUTATIVE.
 GN VC0185.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.
 ON NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Esmolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Uterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae."
 RL Nature 406:477-483(2000).
 DR EMBL: AE004108; AAF93361.1; -;
 DR TIGR: VC0185; -;
 KW Complete proteome.
 SQ SEQUENCE 404 AA; 47642 MW; 26A22EABFCB4BBD CRC64;

Query Match 94.1%; Score 32; DB 16; Length 404;
 Best Local Similarity 83.3%; Pred. No. 78;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYDY 6
 |||||
 Db 273 RKLYDY 278

RESULT 8
 ID P75002 PRELIMINARY; PRT; 433 AA.
 AC P75002;
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR.
 GN GFO.
 OS Zymomonas mobilis.
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 OC Zymomonas.
 ON NCBI_TaxID=542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ZM6;
 RA Wiesert T., Sahn H., Sprenger G.A.;
 *The substitution of a single amino acid residue alters NADP-

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RT containing glucose-fructose oxidoreductase of Zymomonas mobilis . . .";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z80356; CAB02496.1; -.
DR HSSP; 007982; 10R3.
DR InterPro; IPR000683; GFO_IDH_MoCA.
DR InterPro; IPR004104; GFO_IDH_MoCA_C.
DR Pfam; PF01408; GFO_IDH_MoCA; 1.
DR Pfam; PF02894; GFO_IDH_MoCA_C; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 433 AA; 47189 MW; 13CFADE84794E736 CRC64;

Query Match
Best Local Similarity 94.1%; Score 32; DB 2; Length 433;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVDY 6
Db 134 RKLVDY 139

RESULT 9
P91014 PRELIMINARY; PRT; 274 AA.
ID P91014
AC P91014;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOPHETICAL 32.6 KDA PROTEIN.
GN C0168.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Du Z., Gattung S.;
RT "The sequence of C. elegans cosmid C0168.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80439; AAB37641.2; -.
DR HSSP; P25685; 1HDJ.
DR InterPro; IPR003095; DnaJ.
DR InterPro; IPR001623; DnaJ_N.
DR Pfam; PF00226; DnaJ; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 274 AA; 32579 MW; 8A6F3C7692A572E9 CRC64;

Query Match
Best Local Similarity 91.2%; Score 31; DB 5; Length 274;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVDY 6
Db 85 RKLVDY 90

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RESULT 10
Q38198 PRELIMINARY; PRT; 388 AA.
ID Q38198
AC Q38198;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BACTERIOPHAGE CFIC GENE.
OS Xanthomonas phage CfIC.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10862;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91252299; PubMed=1840658;
RA Kuo T.T., Tan M.S., Su M.T., Yang M.K.;
RT "Nucleotide sequence of filamentous phage CfIC from Xanthomonas
RT campestris pv. citri";
RL Nucleic Acids Res. 19:2498-2498(1991).
DR EMBL; M57538; AAA3201.1; -.
SQ SEQUENCE 388 AA; 42785 MW; 4E8ECCE19C0B809 CRC64;

Query Match
Best Local Similarity 91.2%; Score 31; DB 9; Length 388;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVDY 6
Db 155 RKLVDY 160

RESULT 11
Q99TG1 PRELIMINARY; PRT; 409 AA.
ID Q99TG1
AC Q99TG1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SAI524 PROTEIN (MALATE DEHYDROGENASE HOMOLOG).
GN SAI524 OR SAV1702.
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus (strain Mu50).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=158879; 158878;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003134; BAB42791.1; -.
DR EMBL; AP003363; BAB57864.1; -.
DR InterPro; IPR001891; Malic enzyme.
DR InterPro; IPR00205; NAD_binding.
DR Pfam; PF00390; Malic; 2.
DR PRINTS; PR00072; MALOXRDPTASE.
DR PROSITE; PS00331; MALIC_ENZYMES; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 409 AA; 44251 MW; 1D86862B011EBD CRC64;

Query Match
Best Local Similarity 91.2%; Score 31; DB 16; Length 409;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```


QY 1 RKLXYD 6
11:1111
Db 52 RKLYDY 57

RESULT 12

Q45037 PRELIMINARY; PRT; 417 AA.
AC Q45037;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE S1 PROTEIN PRECURSOR.
GN S1.
OS *Borrelia burgdorferi* (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NA0;
RX MEDLINE=95369900; PubMed=7642278;
RA Feng S., Das S., Lam T., Flavell R.A., Fikrig E.;
RT "A 53-kilodalton antigen encoded by a gene on a *Borrelia burgdorferi*
RT 49-kilobase plasmid is recognized by antibodies in sera from patients
RT with Lyme disease.";
RL Infect. Immun. 63:3459-3466(1995).
DR EMBL: L34016; AAA81351.1; -.
KW Signal.
FT SIGNAL. 17
FT CHAIN 18 417 S1 PROTEIN.
SQ SEQUENCE 417 AA; 48869 MW; F691721D194B3D3 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 417;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLXYD 6
11:1111
Db 397 KKLXYD 402

RESULT 13

050899 PRELIMINARY; PRT; 417 AA.
ID 050899;
AC Q50899;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ANTIGEN, S1.
GN BBA05.
OS *Borrelia burgdorferi* (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uitterlind T., Wathey L., McDonald L., Artiach P., Bowman C.,
RA Galand S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*,"
RT Nature 390:580-586(1997).
RL EMBL: AE000790; AAC66229.1; -.
DR TIGR; BBA05; -.
KW Plasmid; Complete proteome.

SQ SEQUENCE 417 AA; 48841 MW; ED6A0FE83A8DDBA CRC64;
Query Match 91.2%; Score 31; DB 16; Length 417;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLXYD 6
11:1111
Db 397 KKLXYD 402

RESULT 14

Q935W7 PRELIMINARY; PRT; 434 AA.
ID Q935W7;
AC Q935W7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ALPHA-ENOOLASE.
GN ENO.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TYPE 2 ATCC 11733;
RA Bergmann S., Rohde M., Chatwal G.S., Hammerschmidt S.;
RT "alpha-enolase of *Streptococcus pneumoniae* is a plasmidogen-binding
RT protein displayed on the bacterial cell surface.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ303085; CAC83091.1; -.
FT CHAIN 2 434 ALPHA-ENOOLASE.
SQ SEQUENCE 434 AA; 47075 MW; 9298639E949F61CE CRC64;

Query Match 91.2%; Score 31; DB 2; Length 434;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLXYD 6
11:1111
Db 253 RKLYDY 258

RESULT 15

Q970S2 PRELIMINARY; PRT; 434 AA.
ID Q970S2;
AC Q970S2;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ENOLASE.
GN SPI128.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radtke D.,
RA Holtzapple E., Khouri H., Wolf A.M., Uitterlind T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of *Streptococcus pneumoniae*,"
RT Science 293:498-506(2001).
RL EMBL: AE007414; AAK75238.1; -.
DR

DR TIGR: SP128; -
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KM Complete proteome.
 SQ SEQUENCE 434 AA; 47103 MW; 0D64F8F04BB99C4 CRC64;
 Query Match 91.2%; Score 31; DB 16; Length 434;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRLYDY 6
 ||:||||
 Db 253 RRYDY 258

Search completed: November 8, 2002, 09:36:12
 Job time : 16.3333 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:36 ; Search time 9 Seconds
(Without alignments)
64.060 Million cell updates/sec

Title: US-09-657-431-11

Perfect score: 34

Sequence: 1 RKLVDY 6

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_71:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	810	1 PLHU	plasmin (EC 3.4.21
2	34	100.0	812	1 PLMS	plasmin (EC 3.4.21
3	32	94.1	73	2 JQ1988	hypothetical 8.5K
4	32	94.1	254	2 B81293	hypothetical prote
5	32	94.1	295	2 S56296	probable membrane
6	32	94.1	404	2 D82355	probable transpos
7	32	94.1	439	2 A42289	glucose-fructose o
8	31	91.2	142	2 A97409	hypothetical prote
9	31	91.2	190	2 E64358	ribosomal protein
10	31	91.2	345	2 T29261	hypothetical prote
11	31	91.2	388	2 S26824	hypothetical prote
12	31	91.2	409	2 B89854	hypothetical prote
13	31	91.2	417	2 E70207	antigen SI - Lyme
14	31	91.2	434	2 E95130	enolase (imported)
15	31	91.2	434	2 D98001	phosphorylative hy
16	31	91.2	522	2 D96602	nucleolar protein
17	31	91.2	1113	2 S73327	MG140 homolog - My
18	31	91.2	1165	2 T30731	probable DNA-direc
19	31	91.2	1404	2 T06663	DNA (cytosine-5-)-
20	31	91.2	1519	2 G71402	DNA (cytosine-5-)-
21	31	91.2	1534	2 S59604	DNA (cytosine-5-)-
22	30	88.2	144	2 S05955	G10 protein - Afri
23	30	88.2	292	2 F95140	tRNA pseudouridine
24	30	88.2	292	2 C98008	pseudouridylate sy
25	30	88.2	314	2 AF0901	tRNA pseudouridine
26	30	88.2	319	2 H97318	transcription regu
27	30	88.2	320	2 T15849	hypothetical prote
28	30	88.2	405	2 T12824	hypothetical prote
29	30	88.2	426	2 C72515	hypothetical prote

30	30	88.2	460	2 B61545
31	30	88.2	474	2 E69481
32	30	88.2	502	2 A82925
33	30	88.2	504	2 S48550
34	30	88.2	647	2 T30892
35	30	88.2	810	2 B30848
36	30	88.2	810	2 I46260
37	30	88.2	959	1 J00017
38	30	88.2	1187	2 C84568
39	30	88.2	1436	2 S67655
40	30	88.2	4548	1 S00657
41	29	85.3	73	2 J01624
42	29	85.3	104	2 G81291
43	29	85.3	117	2 A12440
44	29	85.3	126	2 AE0091
45	29	85.3	177	2 S59643

ALIGNMENTS

RESULT 1
PLHU
plasmin (EC 3.4.21.7) precursor [validated] - human
N:Alternate names: plasminogen precursor [misnomer]
N:Contents: angiotatin; microplasmin; plasminogen
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000
C:Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625;
R:Peterson, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the f
A:Reference number: A35229; MUID:90202879
A:Accession: A35229
A:Molecule type: DNA
A:Residues: 1-810 <PEP>
A:Cross-references: GB:J05286; GB:M4276; NID:q190092; PIDN:AAA36454.1; PID:g387026
A:Experimental source: Leukocyte, lung fibroblast
R:Margaret, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.;
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A:Title: Definition of the transcription initiation site of human plasminogen gene in
A:Reference number: I52242; MUID:91097523
A:Accession: I52242
A:Molecule type: DNA
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <MAL>
A:Cross-references: GB:M62890; NID:q190092; PIDN:AAA36454.1; PID:g553613
R:Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A:Title: Molecular cloning and characterization of a full-length cDNA clone for human
A:Reference number: A26646; MUID:87162490
A:Accession: A26646
A:Molecule type: mRNA
A:Residues: 1-471 'D' 473-810 <FOR>
A:Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531
A:Experimental source: Liver
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A:Title: Characterization of a complementary deoxyribonucleic acid coding for human a
A:Reference number: I45961; MUID:85023311
A:Accession: I62738
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 292-471 'D' 473-810 <MAL>
A:Cross-references: GB:K02922; NID:q190112; PIDN:AAA60123.1; PID:g387031
A:Accession: I84609
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 367-419 <MAL>
A:Cross-references: GB:K02921; NID:q190110; PIDN:AAA60123.1; PID:g190111
R:Brundish, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg,
Eur. J. Biochem. 114, 465-470, 1981
A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of huma

F:79-466/Product: angiotatin #status experimental <AST>
 F:97-580,581-810/Product: plasmin #status experimental <MAT>
 F:97-580/Domains: plasmin chain A #status experimental <CHA>
 F:103-181/Domains: kringle homology <KR1>
 F:185-262/Domains: kringle homology <KR2>
 F:275-352/Domains: kringle homology <KR3>
 F:377-454/Domains: kringle homology <KR4>
 F:481-560/Domains: kringle homology <KR5>
 F:550-580,581-810/Product: microplasmin #status experimental <MMT>

Query Match 100.0%; Score 34; DB 1; Length 810;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYDY 6
 DB 549 RKLYDY 554

RESULT 2

PLMS
 N:Contains: angiotatin; plasminogen
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
 C:Accession: A38514; S48202; S48203
 R:Degeen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
 Genomics 8, 49-61, 1990
 A:Title: Characterization of the cDNA coding for mouse plasminogen and localization of
 A:Reference number: A38514; MUID:91184812
 A:Accession: A38514

A:Molecule type: mRNA
 A:Residues: 1-812 <DEG>
 A:Cross-references: GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g200403
 R:Liljenn, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
 Eur. J. Biochem. 224, 863-871, 1994
 A:Title: Characterization of the murine plasma fibrinolytic system.
 A:Reference number: S48202; MUID:95010076
 A:Accession: S48202

A:Molecule type: protein
 A:Residues: 20-25 <LIU>
 A:Accession: S48203

A:Molecule type: protein
 A:Residues: 22-27 <LI2>
 C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many of
 C:Comment: plasminogen is converted into plasmin by plasminogen activators, both plasmin
 immediately after dissociation from the clot. In the presence of the inhibitor, the activa
 e inhibitor, the activation involves also removal of the activation peptide.
 C:Comment: Streptolysin I (see PIR:KCMS1) acts on plasminogen to produce angiotatin. TC
 eful in treating solid tumors.

C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd
 F:1-96/Domains: plasminogen-related protein precursor homology <PLPH>
 F:1-18/Domains: signal sequence #status predicted <SIG>
 F:20-812/Product: plasminogen #status predicted <PRO>
 F:20-96/Domains: activation peptide #status predicted <APT>
 F:79-466/Product: angiotatin #status predicted <AST>
 F:97-581,582-812/Product: plasmin #status predicted <MAT>
 F:97-581/Domains: chain A #status predicted <ACH>
 F:103-181/Domains: kringle homology <KR1>
 F:185-262/Domains: kringle homology <KR2>
 F:275-352/Domains: kringle homology <KR3>
 F:377-454/Domains: kringle homology <KR4>
 F:481-560/Domains: kringle homology <KR5>
 F:582-812/Domains: chain B #status predicted <BCH>
 F:582-805/Domains: trypsin homology <TRY>
 F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
 bonds: #status predicted
 F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted

F:136,308/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted
 F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
 F:624,667,765/Active site: His, Asp, Ser #status predicted

Query Match 100.0%; Score 34; DB 1; Length 812;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYDY 6
 DB 549 RKLYDY 554

RESULT 3

J01988
 N:Alternate names: ORF 2 protein
 C:Species: turkey rhinotracheitis virus
 C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
 C:Accession: J01988
 R:Yu, Q.; Davis, P.J.; Brown, T.D.K.; Cavanagh, D.
 J. Gen. Virol. 73, 1353-1363, 1992
 A:Title: Sequence and in vitro expression of the M2 gene of turkey rhinotracheitis pn
 A:Reference number: J01987; MUID:92300329
 A:Accession: J01988
 A:Molecule type: mRNA
 A:Residues: 1-73 <YUO>
 A:Cross-references: GB:X63408; NID:g297846; PIDN:CAA5005.1; PID:g297848

Query Match 94.1%; Score 32; DB 2; Length 73;
 Best Local Similarity 83.3%; Pred. No. 8.6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYDY 6
 DB 25 RKLYDY 30

RESULT 4

B81293
 N:hypothetical protein Cj1467 [imported] - Campylobacter jejuni (strain NCTC 11168)
 C:Species: Campylobacter jejuni
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
 C:Accession: B81293
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chl
 C.W.; Quail, M.; Randleman, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Ba
 Nature 403, 665-668, 2000
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
 A:Reference number: A81250; MUID:20150912
 A:Accession: B81293

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-254 <PAR>
 A:Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73890.1; PID:g696
 A:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:
 A:Gene: Cj1467

Query Match 94.1%; Score 32; DB 2; Length 254;
 Best Local Similarity 83.3%; Pred. No. 31;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYDY 6
 DB 210 RKLYDY 215

RESULT 5

S56296
 N:Alternate names: hypothetical protein F018
 C:Species: Saccharomyces cerevisiae

C:Date: 02-Sep-1995 #sequence-revision 19-Oct-1995 #text-change 05-Dec-1997
 C:Accession: S56296; S62252; S63788
 R:Murakami, Y.; Naitou, M.; Hagihara, H.; Shibata, T.; Ozawa, M.; Sasamura, S.I.; Sasano, submitted to the EMBL Data Library, May 1995
 A:Description: Analysis of the nucleotide sequence of chromosome VI from *Saccharomyces cerevisiae*
 A:Reference number: S56186
 A:Accession: S56296
 A:Molecule type: DNA
 A:Residues: 1-295 <MUR>
 A:Cross-references: EMBL:D50617; NID:9836685; PID:d1009921; PID:9836796; MIPS:YFR041C
 R:Murakami, Y.
 Submitted to the EMBL Data Library, December 1994
 A:Reference number: S62230
 A:Accession: S62252
 A:Molecule type: DNA
 A:Residues: 1-295 <MUR>
 A:Cross-references: EMBL:D44597; NID:9871938; PID:d1008597; PID:9871940
 R:Ekl, T.; Naitou, M.; Hagihara, H.; Ozawa, M.; Sasamura, S.I.; Tsuchiya, Y.
 Yeast 12, 149-167, 1996
 A:Title: Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome VI
 A:Reference number: S63787; MUID:96287652
 A:Accession: S63788
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-295 <EKL>
 A:Cross-references: EMBL:D44597; NID:9871938; PID:d1008597; PID:9871940
 C:Genetics:
 A:Map position: 6R
 A:Note: YFR041C
 C:Superfamily: dnaJ amino-terminal homology
 C:Keywords: transmembrane protein
 F:8-24/Domain: transmembrane #status predicted <TM1>
 F:44-108/Domain: dnaJ amino-terminal homology <DNJ>
 F:133-149/Domain: transmembrane #status predicted <TM2>

Query Match
 Best Local Similarity 94.1%; Score 32; DB 2; Length 295;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RKLYDY 6
 ||:||||
 Db 101 RKLYDY 106

RESULT 6
 D82355
 Probable transposase VC0185 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
 C:Species: *Vibrio cholerae*
 C:Date: 18-Aug-2000 #sequence-revision 20-Aug-2000 #text-change 02-Feb-2001
 C:Accession: D82355
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chaudson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Olin, H.; Dragoti, I.; Sellers, F.L.; R.K.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A:Reference number: A82035; MUID:20406833
 A:Accession: D82355
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-404 <HEI>
 A:Cross-references: GB:AE004108; GB:AE003852; NID:99654578; PIDN:AAF93361.1; GSPDB:GN001
 A:Experimental source: serogroup O1, strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC0185
 A:Map position: 1
 C:Superfamily: *Vibrio cholerae* probable transposase VC0185

Query Match
 Best Local Similarity 94.1%; Score 32; DB 2; Length 404;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RKLYDY 6
 ||:||||

Db 273 RKMTDY 278

RESULT 7
 A42289
 glucose-fructose oxidoreductase (EC 1.1.-.-) precursor - *Zymomonas mobilis*
 C:Species: *Zymomonas mobilis*
 C:Date: 10-Jul-1992 #sequence-revision 10-Jul-1992 #text-change 08-Oct-1999
 C:Accession: A42289
 R:Kanasundaram, V.; Scopes, R.R.
 J. Bacteriol. 174, 1439-1447, 1992
 A:Title: Cloning, sequence analysis, and expression of the structural gene encoding g
 A:Reference number: A42289; MUID:92165717
 A:Accession: A42289
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-439 <KAN>
 A:Cross-references: GB:M97379; NID:9155587; PIDN:AAA27690.1; PID:9155588
 C:Keywords: oxidoreductase

Query Match
 Best Local Similarity 94.1%; Score 32; DB 2; Length 439;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RKLYDY 6
 ||:||||
 Db 133 RKLYDY 138

RESULT 8
 A97409
 hypothetical protein AGR_C-723 [imported] - *Agrobacterium tumefaciens* (strain C58, Ce
 C:Species: *Agrobacterium tumefaciens*
 C:Date: 30-Sep-2001 #sequence-revision 30-Sep-2001 #text-change 11-Jan-2002
 C:Accession: A97409
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouello, B.; Gold
 A.; Liu, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium*
 A:Reference number: A97359; PMID:11743194
 A:Accession: A97409
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-142 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK86226.1; PID:915155328; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C-723
 A:Map position: circular chromosome

Query Match
 Best Local Similarity 91.2%; Score 31; DB 2; Length 142;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RKLYDY 6
 ||:||||
 Db 129 RKLYDY 134

RESULT 9
 E64358
 ribosomal protein L5 - *Methanococcus jannaschii*
 C:Species: *Methanococcus jannaschii*
 C:Date: 13-Sep-1996 #sequence-revision 13-Sep-1996 #text-change 21-Jul-2000
 C:Accession: E64358
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
 ; Reich, C.T.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,
 son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
 A:Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*
 A:Reference number: A64300; MUID:96337999
 A:Accession: E64358
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-190 <BU>
A:Cross-references: GB:U67497; GB:L77117; NID:g2826284; PIDN:AB98458.1; PID:g1591171;
C:Genetics:
A:Map position: FOR415069-415641
C:Superfamily: Escherichia coli ribosomal protein L5

Query Match 91.2%; Score 31; DB 2; Length 190;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLXDY 6
:|||||
Db 95 RKLXDY 100

RESULT 10

T29261
hypothetical protein C01G8.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29261
R:Du. 2; Gattung S.
Submitted to the EMBL Data Library, November 1996
A:Description: The sequence of C. elegans cosmid C01G8.
A:Reference number: 220597
A:Accession: T29261
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-345 <DU>
A:Cross-references: EMBL:U80439; PIDN:AB37641.1; GSPDB:GN00019; CESP:C01G8.4
A:Experimental source: strain Bristol N2; clone C01G8
C:Genetics:
A:Gene: CESP:C01G8.4
A:Map position: 1
A:introns: 18/2; 54/3; 80/2; 119/2; 169/2; 207/3

Query Match 91.2%; Score 31; DB 2; Length 345;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLXDY 6
:|||||
Db 85 RKLXDY 90

RESULT 11

S26824
hypothetical protein - phage CflC
C:Species: phage CflC
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
C:Accession: S26824
R:Kuo, T.T.; Tan, M.S.; Su, M.T.; Yang, M.K.
Nucleic Acids Res. 19, 2498, 1991
A:Title: Complete nucleotide sequence of filamentous phage CflC from Xanthomonas campestris
A:Reference number: S26824; MUID:91252299
A:Accession: S26824
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-388 <KU>
A:Cross-references: EMBL:M57538; NID:g166169; PIDN:AAA32201.1; PID:g166170
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1991

Query Match 91.2%; Score 31; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLXDY 6
:|||||
Db 155 RKLXDY 160

RESULT 12

B89954
hypothetical protein SA1524 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: B89954
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shib, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89954
A:Status: preliminary
A:Accession: B89954
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <KUR>
A:Cross-references: GB:BA000018; PID:g13701497; PIDN:BA842791.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1524
C:Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)

Query Match 91.2%; Score 31; DB 2; Length 409;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLXDY 6
:|||||
Db 52 RKLXDY 57

RESULT 13

E70207
antigen S1 - Lyme disease spirochete plasmid A/1p54
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C:Accession: E70207; 140296
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh
son, D.; Peterson, J.; Kervatage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
Boman, C.; Garland, S.; Fujil, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943
A:Accession: E70207
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-417 <KLE>
A:Cross-references: GB:AE000790; NID:g2690224; PIDN:AC66229.1; PID:g2690228; TIGR:BB
A:Experimental source: strain B31
R:Feng, S.; Das, S.; Lam, T.; Flavell, R.A.; Fikrig, E.
Infect. Immun. 63, 3459-3466, 1995
A:Title: A 55-kilodalton antigen encoded by a gene on a Borrelia burgdorferi 49-kilob
A:Reference number: 140296; MUID:95369900
A:Accession: 140296
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18, 'R', 20-417 <RES>
A:Cross-references: GB:U34016; NID:g1063416; PIDN:AA81351.1; PID:g1063417
A:Experimental source: strain N40
C:Genetics:
A:Gene: S1
A:Genome: plasmid

Query Match 91.2%; Score 31; DB 2; Length 417;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLXDY 6
:|||||
Db 397 RKLXDY 402

RESULT 14

```

E95130
enolase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: E95130
R:Jettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Held
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfe,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95130
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-434 <KUR>
A:Cross-References: GB:AE005672; PIDN:AAK5238.1; PTD:914972605; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP1128
C:Superfamily: enolase

Query Match          91.2%  Score 31;  DB 2;  Length 434;
Best Local Similarity 83.3%  Pred. No. 85;
Matches 5;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1 RKLYDY 6
||:||||
Db 253 RKVYDY 258

RESULT 15
D98001
phosphopyruvate hydratase (EC 4.2.1.11) [imported] - Streptococcus pneumoniae (strain R6
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: D98001
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, I.N.; Letkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: D98001
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-434 <KUR>
A:Cross-References: GB:AE007317; PIDN:AAK99840.1; PTD:915458655; GSPDB:GN00174
C:Genetics:
A:Gene: eno
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match          91.2%  Score 31;  DB 2;  Length 434;
Best Local Similarity 83.3%  Pred. No. 85;
Matches 5;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1 RKLYDY 6
||:||||
Db 253 RKVYDY 258

```

Search completed: November 8, 2002, 09:36:45
 Job time : 10 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2002, 09:34:41 ; Search time 30 Seconds
(without alignments)
22.215 Million cell updates/sec

Title: US-09-657-431-11

Perfect score: 6
Sequence: 1 RKLXDY 6

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A_Geneseq_032802:*

1:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	100.0	6	18 AAW34302	Kringle 5 peptide
2	6	100.0	6	21 AAB01903	Human plasminogen
3	6	100.0	6	22 AAB92098	Laminin fragment S
4	6	100.0	6	22 AAB36572	Mammalian kringle
5	6	100.0	6	18 AAW34303	Kringle 5 peptide
6	6	100.0	6	18 AAW34304	Kringle 5 peptide
7	6	100.0	6	18 AAW34306	Kringle 5 peptide
8	6	100.0	6	18 AAW34299	Kringle 5 peptide
9	6	100.0	6	18 AAW34290	Human kringle 5 pe
10	6	100.0	6	18 AAW34291	Human kringle 5 pe
11	6	100.0	6	21 AAB01888	Human plasminogen

12	6	100.0	7	21 AAB01889	Human plasminogen
13	6	100.0	7	21 AAB01900	Human plasminogen
14	6	100.0	7	22 AAB92097	Laminin fragment S
15	6	100.0	7	22 AAB36571	Mammalian kringle
16	6	100.0	7	22 AAB36576	Mammalian kringle
17	6	100.0	8	22 AAB83292	Kringle peptide #1
18	6	100.0	8	22 AAB92092	Laminin fragment S
19	6	100.0	8	22 AAB92101	Laminin fragment S
20	6	100.0	8	22 AAB36567	Mammalian kringle
21	6	100.0	8	22 AAB36575	Mammalian kringle
22	6	100.0	11	18 AAW34298	Kringle 5 peptide
23	6	100.0	11	21 AAB01899	Human plasminogen
24	6	100.0	11	22 AAB92094	Laminin fragment S
25	6	100.0	11	22 AAB36569	Mammalian kringle
26	6	100.0	12	22 AAB92089	Laminin fragment S
27	6	100.0	12	22 AAB92093	Laminin fragment S
28	6	100.0	12	22 AAB36564	Mammalian kringle
29	6	100.0	12	22 AAB36568	Mammalian kringle
30	6	100.0	21	21 AAB15521	Sequences flanking
31	6	100.0	23	22 AAB83293	Kringle peptide #2
32	6	100.0	23	22 AAB92096	Laminin fragment S
33	6	100.0	23	22 AAB36570	Mammalian kringle
34	6	100.0	24	22 AAB92090	Laminin fragment S
35	6	100.0	24	22 AAB92095	Laminin fragment S
36	6	100.0	24	22 AAB36565	Mammalian kringle
37	6	100.0	79	18 AAW19256	Human plasminogen
38	6	100.0	85	21 AAB08413	Amino acid sequenc
39	6	100.0	90	21 AAB01914	Human plasminogen
40	6	100.0	91	21 AAT58868	Human plasminogen
41	6	100.0	93	21 AAB01917	Human plasminogen
42	6	100.0	95	21 AAB01913	Human plasminogen
43	6	100.0	98	21 AAB01916	Human plasminogen
44	6	100.0	101	18 AAW34286	Human kringle 5 pe
45	6	100.0	101	21 AAB01890	Human plasminogen

ALIGNMENTS

RESULT 1					
ID	AAW34302	standard;	peptide:	6 AA.	
XX	AAW34302:				
XX	14-MAY-1998	(first entry)			
DT		Kringle 5 peptide fragment.			
DE					
XX		Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;			
KW		metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;			
KW		psoriasis; arthritis; macular degeneration; diabetic retinopathy;			
KW		autoimmune disease; ocular disease; capillary proliferation; therapy;			
OS		Kringle 5 receptor.			
XX		Synthetic.			
XX					
FT	Key	Location/Qualifiers			
FT	Modified-site	1 /note= "N-Ac-Arg"			
FT	Modified-site	6 /note= "C-terminal amide"			
PA	WO9741824-A2.				
PN	13-NOV-1997.				
PD					
XX	05-MAY-1997;	97WO-US07700.			
XX	03-APR-1997;	97US-0832087.			
PR	03-MAY-1996;	96US-0643219.			
XX					
PA	(ABBO) ABBOTT LAB.				

XX Davidon DJ, Gubbins EJ, Wang J;
PI WPI; 1997-558670/51.
XX

PT New kringle 5 peptide(s) and fusion proteins derived from
PT plasminogen - useful as anti-angiogenesis agents for treating
PT cancer, psoriasis, arthritis etc., including gene therapy
XX

PS Example 9; Page 45; 78pp: English.

CC This sequence is synthetic a kringle 5 (K5) peptide homologous to human
CC plasminogen. K5 peptide fragments homologous to this sequence, are
CC anti-angiogenesis agents, specifically for treating or preventing cancer,
CC particularly primary or metastatic solid tumours, carcinomas, sarcomas,
CC lymphomas, haemangiomas. They can also be used for treating or preventing
CC psoriasis, arthritis, macular degeneration and diabetic retinopathy. The
CC fragments can also be used to treat autoimmune or ocular diseases,
CC capillary proliferation within atherosclerotic plaque, haemophilic
CC joints, wound granulation, ulcers etc., also as contraceptives that
CC inhibit ovulation and establishment of the placenta. K5 antisera or
CC (ant)agonists can be used similarly, optionally coupled to cytotoxic
CC agents. Antagonists may be used to induce angiogenesis, e.g. for wound
CC healing. The K5 peptides are also used to raise specific antibodies (Ab),
CC for diagnosis and for affinity purification of K5 receptors. The K5
CC receptors may then be expressed in tumour cells to increase their
CC response to the peptides or used for identification of smaller
CC antagonists. The Ab are used to detect/quantify the peptides in
CC biological samples. The K5 peptides (and K5 fusion proteins) selectively
CC inhibit proliferation of endothelial cells with low toxicity against
CC normal cells. Typically they have 800-times greater inhibitory activity
CC against bovine capillary cells in vitro than kringle 1-4 peptides.

XX Sequence 6 AA;

Query Match 100.0%; Score 6; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
|||||
Db 1 RKLYDY 6

RESULT 2

AAB01903
ID AAB01903 standard; peptide; 6 AA.

AC AAB01903;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringle 5 peptide fragment #9.

KW Plasminogen: human; kringle 5 domain; endothelial cell proliferation;
KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
KW antipsoriatic; antiinflammatory; antitumor; antineurotic; antiarthritic;
KW antiangiogenic; cancer; tumour; autoimmune disease.

XX Homo sapiens.
OS
XX

FT Key

FT Modified-site 1 Location/Qualifiers

FT Modified-site 6 /note= "N-terminal acetyl moiety"

FT Modified-site 6 /note= "C-terminal amide moiety"

PN US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

XX

PR 03-MAY-1996; 96US-0643219.
PR 03-APR-1997; 97US-0832087.

PA (ABBO) ABBOTT LAB.

PI Davidon DJ;

DR WPI; 2000-349573/30.

PT Preparation of kringle five peptide fragment for treating various
PT disorders such as angiogenic, ocular, skin diseases and cancer,
PT involves mixing mammalian plasminogen and elastase followed by
PT incubation and isolation -

PS Example 9; Column 37; 48pp: English.

CC The invention relates to a method of preparing plasminogen kringle 5
CC peptide fragments. The method comprises mixing mammalian plasminogen and
CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
CC endothelial cell proliferation and migration. The peptides are useful
CC for treating angiogenic diseases, primary and metastatic solid tumours
CC and carcinomas of various organs such as breast, genital tract,
CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
CC arising from haematopoietic malignancies such as leukemias and
CC lymphomas. They are also used for the prophylaxis of various autoimmune
CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
CC (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber
CC Syndrome), diseases caused by excessive or abnormal stimulation of
CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
CC disease and ulcers). The peptides are also useful as a birth control
CC agent which inhibits ovulation and establishment of the placenta.
CC Sequences AAB01888, AAB01889 and AAB01895-B01905 represent human
CC plasminogen kringle 5-derived peptides synthesised and used in
CC exemplifications of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 6; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
|||||
Db 1 RKLYDY 6

RESULT 3

AAB92098
ID AAB92098 standard; Peptide; 6 AA.

AC AAB92098;

DT 22-JUN-2001 (first entry)

DE Laminin fragment SEQ ID NO:1274.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
OS
XX

FT Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000MO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

15-0CT-1999; 99US-0159783.
(CONU-) CONUICHEM INC.
Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
WPI: 2001-112059/12.
Modifying and attaching therapeutic peptides to albumin prevents
peptidase degradation, useful for increasing length of in vivo activity
-
Disclosure: Page 612; 733pp; English.
The present invention describes a modified therapeutic peptide (I)
comprising a therapeutically active amino acid region (III) and a
reactive group (II) (e.g. succinimidy] and maleimido groups) attached to
a less therapeutically active amino acid region (IV), which covalently
bonds with amino/thiol groups on blood components to form a
peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
(I) are useful for modifying therapeutic peptides e.g. hormones, growth
factors and neurotransmitters, to protect them from peptidase activity
in vivo for the treatment of various disorders. Endogenous therapeutic
peptides are not suitable as drug candidates as they require frequent
administration due to rapid degradation by peptidases in the body.
Modifying and attaching therapeutic peptides to albumin prevents or
reduces the action of peptidases to increase length of activity (half
life) and specificity as bonding to large molecules decreases
intracellular uptake and interference with physiological processes.
AAB90829 to AAB92441 represent peptides which can be used in the
exemplification of the present invention.

Sequence 6 AA;

Query Match	100.0%;	Score 6;	DB 22;	Length 6;
Best Local	Similarity	100.0%;	Pred. No. 6.4e+05;	
Matches	6; Conservative	0;	Mismatches	0; Gaps 0

QY	1	RKLYDY	6
Db	1	RKLYDY	6

RESULT 4
AAB36572

ID AAB36572 standard; Peptide; 6 AA.

AC AAB36572;

DT 09-MAR-2001 (first entry)

DE Mammalian kringle 5 peptide SEQ ID NO:11

[illegible]

OS Mammalia:

PN WO2000070665-A2

PD 23-NOV-2000

PF 17-MAY-2000; 2000WO-IB00763

PR 17-MAY-1999; 99US-0134406

PA (CONJ-) CONJUCHEM INC

XX Bridon DP, Rasamceliso M, Thiabdeau K, Huang X, Bellevue R
PI
XX WPI; 2001-090970/10.
DR

WPI; 2001-090970/10.

PT New modified anti-angiogenic kringle 5 peptides capable of forming
PT conjugates with blood proteins, useful for treating angiogenesis,
PT inappropriate invasion of vessels or cancers in humans or mammals
XX
PS Claim 6; Page 9; 82pp; English.

Claim 6; Page 9; 82pp; English

The present invention describes a modified anti-angiogenic peptide (I) comprising a reactive group that reacts with amino groups, hydroxyl groups or thiol groups on blood components to form stable covalent bonds. The reactive group is selected from succinimidy or maleimido groups. (I) can have anti-inflammatory, vasotropic, cytostatic, anti-neurathic, antipsoriatic, antidiabetic, antiarteriosclerotic and osteoprotactic activities, and is an angiogenesis inhibitor. (I) are useful for treating angiogenesis in a human, where the derivative is reacted with blood proteins. (I) are also useful for manufacturing a medicament extending the in vivo half-life of a kringle 5 peptide in a patient to provide an anti-angiogenic effect. In particular, a modified kringle 5 peptide can be used for treating inflammatory disorders (e.g. immune and non-immune inflammation, chronic articular rheumatism or psoriasis), disorders associated with inappropriate or inopportune invasion of vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis), capillary proliferation in atherosclerotic plaques or osteoporosis), or cancer associated disorders (e.g. solid tumours, solid tumour metastases, angiofibromas, retrolental fibroplasia, haemangiomas, Kaposi's sarcoma or other cancers requiring neovascularisation to support tumour growth). The peptides are useful for treating these diseases in mammalian or human patients. AAB36562 represents a mammalian kringle 5 protein, and AAB36563 to AAB36577 represent specifically claimed kringle 5 peptides from the present invention.

Sequence 6 AA;

Query Match	100.0%	Score	22	DB	22	Length	6
Best Local Similarity	100.0%	Pred. No.	6.4e+05				
Matches	6	Conservative	0	Mismatches	0	Indels	0
						Gaps	0

QY	1	RKLYDY	6
Db	1	RKLYDY	6

RESULT 5
AAW34303

ID AAW34303 standard; peptide; 7 AA.

AC AAW34303;

DT 14-MAY-1998 (first entry)

DE Kringle 5 peptide fragment.

KW Plasminogen; human; kringle 5 peptide; anti-angiogenesis agent; cancer
KW metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
KW psoriasis; arthritis; macular degeneration; diabetic retinopathy;
KW autoimmune disease; ocular disease; capillary proliferation; therapy;
KW kringle 5 receptor.

OS Synthetic

Key	Location/Qualifiers
FH	
...	

/note= "N-Ac-Pro"

```

7 /note= "3-I-tyrosyl"
ET

```

/note= "C-terminal amide

PN W09741824-A2.

XX 13-NOV-1997.
 PD 05-MAY-1997; 97WO-US07700.
 PF 03-APR-1997; 97US-0832087.
 PR 03-MAY-1996; 96US-0643219.
 XX (ABBO) ABBOTT LAB.
 PA Davidson DJ, Gubbins EJ, Wang J;
 PI WPI, 1997-558670/51.
 DR
 XX
 XX New kringle 5 peptide(s) and fusion proteins derived from
 PT plasminogen - useful as anti-angiogenesis agents for treating
 PT cancer, psoriasis, arthritis etc., including gene therapy
 XX
 PS Example 10; Page 45; 78pp; English.
 XX
 CC This sequence is synthetic a kringle 5 (K5) peptide homologous to human
 CC plasminogen. K5 peptide fragments homologous to this sequence, are
 CC anti-angiogenesis agents, specifically for treating or preventing cancer,
 CC particularly primary or metastatic solid tumours, carcinomas, sarcomas,
 CC lymphomas, haemangiomas. They can also be used for treating or preventing
 CC psoriasis, arthritis, macular degeneration and diabetic retinopathy. The
 CC fragments can also be used to treat autoimmune or ocular diseases.
 CC capillary proliferation within atherosclerotic plaque, haemophilic
 CC joints, wound granulation, ulcers etc., also as contraceptives that
 CC inhibit ovulation and establishment of the placenta. K5 antisera or
 CC (ant)agonists can be used similarly, optionally coupled to cytotoxic
 CC agents. Antagonists may be used to induce angiogenesis, e.g. for wound
 CC healing. The K5 peptides are also used to raise specific antibodies (Ab),
 CC for diagnosis and for affinity purification of K5 receptors. The K5
 CC receptors may then be expressed in tumour cells to increase their
 CC response to the peptides or used for identification of smaller
 CC antagonists. The Ab are used to detect/quantify the peptides in
 CC biological samples. The K5 peptides (and K5 fusion proteins) selectively
 CC inhibit proliferation of endothelial cells with low toxicity against
 CC normal cells. Typically they have 800-times greater inhibitory activity
 CC against bovine capillary cells in vitro than kringle 1-4 peptides.
 XX
 SQ Sequence 7 AA:
 Query Match 100.0%; Score 6; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKLYDY 6
 DB 2 RKLYDY 7
 RESULT 6
 AAW34304
 ID AAW34304 standard; peptide; 7 AA.
 XX
 AC AAW34304;
 XX
 DT 14-MAY-1998 (first entry)
 XX
 DE Kringle 5 peptide fragment.
 XX
 KW Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
 KW metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
 KW psoriasis; arthritis; macular degeneration; diabetic retinopathy;
 KW autoimmune disease; ocular disease; capillary proliferation; therapy;
 KW kringle 5 receptor.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1

FT /note= "N-Ac-Pro"
 FT Modified-site 7
 FT /note= "3-I-Tyrosyl"
 FT Modified-site 7
 FT /note= "C-terminal amide"
 XX
 XX W09741824-A2.
 PD 13-NOV-1997.
 PA 05-MAY-1997; 97WO-US07700.
 PF 03-APR-1997; 97US-0832087.
 PR 03-MAY-1996; 96US-0643219.
 XX (ABBO) ABBOTT LAB.
 PA Davidson DJ, Gubbins EJ, Wang J;
 PI WPI, 1997-558670/51.
 DR
 XX
 XX New kringle 5 peptide(s) and fusion proteins derived from
 PT plasminogen - useful as anti-angiogenesis agents for treating
 PT cancer, psoriasis, arthritis etc., including gene therapy
 XX
 PS Example 11; Page 45; 78pp; English.
 XX
 CC This sequence is synthetic a kringle 5 (K5) peptide homologous to human
 CC plasminogen. K5 peptide fragments homologous to this sequence, are
 CC anti-angiogenesis agents, specifically for treating or preventing cancer,
 CC particularly primary or metastatic solid tumours, carcinomas, sarcomas,
 CC lymphomas, haemangiomas. They can also be used for treating or preventing
 CC psoriasis, arthritis, macular degeneration and diabetic retinopathy. The
 CC fragments can also be used to treat autoimmune or ocular diseases,
 CC capillary proliferation within atherosclerotic plaque, haemophilic
 CC joints, wound granulation, ulcers etc., also as contraceptives that
 CC inhibit ovulation and establishment of the placenta. K5 antisera or
 CC (ant)agonists can be used similarly, optionally coupled to cytotoxic
 CC agents. Antagonists may be used to induce angiogenesis, e.g. for wound
 CC healing. The K5 peptides are also used to raise specific antibodies (Ab),
 CC for diagnosis and for affinity purification of K5 receptors. The K5
 CC receptors may then be expressed in tumour cells to increase their
 CC response to the peptides or used for identification of smaller
 CC antagonists. The Ab are used to detect/quantify the peptides in
 CC biological samples. The K5 peptides (and K5 fusion proteins) selectively
 CC inhibit proliferation of endothelial cells with low toxicity against
 CC normal cells. Typically they have 800-times greater inhibitory activity
 CC against bovine capillary cells in vitro than kringle 1-4 peptides.
 XX
 SQ Sequence 7 AA:
 Query Match 100.0%; Score 6; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKLYDY 6
 DB 2 RKLYDY 7
 RESULT 7
 AAW34306
 ID AAW34306 standard; peptide; 7 AA.
 XX
 AC AAW34306;
 XX
 DT 14-MAY-1998 (first entry)
 XX
 DE Kringle 5 peptide fragment.
 XX
 KW Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
 KW metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
 KW psoriasis; arthritis; macular degeneration; diabetic retinopathy;

KM		autoimmune disease; ocular disease; capillary proliferation; therapy;
XW		kringle 5 receptor.
XX		Synthetic.
OS		
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	1
FT	Modified-site	/note= "N-Ac-Pro"
FT	Modified-site	7
FT	Modified-site	/note= "3-I-tyrosyl"
FT	Modified-site	7
FT	Modified-site	/note= "C-terminal amide"
XX		
PN	WO9741824-A2.	
XX		
PD	13-NOV-1997.	
XX		
PF	05-MAY-1997;	97WO-US07700.
XX		
PR	03-APR-1997;	97US-0832087.
PR	03-MAY-1996;	96US-0643219.
XX		
PA	(ABBO) ABBOTT LAB.	
XX		
PI	Davidson DJ, Gubblins EJ, Wang J;	
DR	WPI, 1997-558670/51.	
XX		
PT	New kringle 5 peptide(s) and fusion proteins derived from plasminogen - useful as anti-angiogenesis agents for treating cancer, psoriasis, arthritis etc., including gene therapy	
PT		
PS	Example 13; Page 46; 78pp; English.	
XX		
CC	This sequence is synthetic a kringle 5 (K5) peptide homologous to human plasminogen. K5 peptide fragments homologous to this sequence, are anti-angiogenesis agents, specifically for treating or preventing cancer, particularly primary or metastatic solid tumours, carcinomas, sarcomas, lymphomas, haemangiomias. They can also be used for treating or preventing psoriasis, arthritis, macular degeneration and diabetic retinopathy. The fragments can also be used to treat autoimmune or ocular diseases, capillary proliferation within atherosclerotic plaque, hemophilic joints, wound granulation, ulcers etc., also as contraceptives that inhibit ovulation and establishment of the placenta. K5 antisera or (ant)agonists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce angiogenesis, e.g. for wound healing. The K5 peptides are also used to raise specific antibodies (Ab), for diagnosis and for affinity purification of K5 receptors. The K5 receptors may then be expressed in tumour cells to increase their response to the peptides or used for identification of smaller antagonists. The Ab are used to detect/quantify the peptides in biological samples. The K5 peptides (and K5 fusion proteins) selectively inhibit proliferation of endothelial cells with low toxicity against normal cells. Typically they have 800-times greater inhibitory activity against bovine capillary cells in vitro than kringle 1-4 peptides.	
XX		
SQ	Sequence	7 AA;
	Query Match	100.0%; Score 6; DB 18; Length 7;
	Best Local Similarity	100.0%; Pred. No. 6.4e+05;
	Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.0;
OY	1 RRLTYD 6	
Db	2 RRLTYD 7	
RESULT 8		
AAM34299	ID	AAM34299 standard; peptide; 7 AA.
AC		
AAW34299;		

DT	14-MAY-1998	(first entry)
XX		
DE	Kringle 5 peptide fragment.	
KW	Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;	
KW	metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;	
KW	psoriasis; arthritis; macular degeneration; diabetic retinopathy;	
KW	autoimmune disease; ocular disease; capillary proliferation; therapy;	
KW	kringle 5 receptor.	
XX		
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	Modified-site	1
FT		/note= "N-Ac-Pro"
FT	Modified-site	7
FT		/note= "C-terminal amide"
XX		
PN	W09741824-A2.	
XX		
PD	13-NOV-1997.	
XX		
PE	05-MAY-1997;	97WO-US07700.
XX		
PR	03-APR-1997;	97US-0832087.
XX		
PR	03-MAY-1996;	96US-0643219.
XX		
PA	(ABBO) ABBOTT LAB.	
PI		
PI	Davidson DJ, Gubbins EJ, Wang J;	
XX		
DR	WPI; 1997-558670/51.	
XX		
PT	New kringle 5 peptide(s) and fusion proteins derived from	
PT	plasminogen - useful as anti-angiogenesis agents for treating	
PT	cancer, psoriasis, arthritis etc., including gene therapy	
XX		
PS	Example 6; Page 44; 78pp; English.	
XX		
CC	This sequence is synthetic a kringle 5 (K5) peptide homologous to human	
CC	plasminogen. K5 peptide fragments homologous to this sequence, are	
CC	anti-angiogenesis agents, specifically for treating or preventing cancer,	
CC	particularly primary or metastatic solid tumours, carcinomas, sarcomas,	
CC	lymphomas, haemangiomas. They can also be used for treating or preventing	
CC	psoriasis, arthritis, macular degeneration and diabetic retinopathy. The	
CC	fragments can also be used to treat autoimmune or ocular diseases,	
CC	capillary proliferation within atherosclerotic plaque, haemophilic	
CC	joints, wound granulation, ulcers etc., also as contraceptives that	
CC	inhibit ovulation and establishment of the placenta. K5 antisera or	
CC	(ant)agonists can be used similarly, optionally coupled to cytotoxic	
CC	agents. Antagonists may be used to induce angiogenesis, e.g. for wound	
CC	healing. The K5 peptides are also used to raise specific antibodies (Ab),	
CC	for diagnosis and for affinity purification of K5 receptors. The K5	
CC	receptors may then be expressed in tumour cells to increase their	
CC	response to the peptides or used for identification of smaller	
CC	antagonists. The Ab are used to detect/quantify the peptides in	
CC	biological samples. The K5 peptides (and K5 fusion proteins) selectively	
CC	inhibit proliferation of endothelial cells with low toxicity against	
CC	normal cells. Typically they have 800-times greater inhibitory activity	
CC	against bovine capillary cells in vitro than Kringle 1-4 peptides.	
XX		
XX		
SQ	Sequence 7 AA;	
QY	Query Match	100.0%; Score 6; DB 18; Length 7;
DB	Best Local Similarity	100.0%; Pred. No. 6.4e+05;
	Matches 6; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
	1 RKLVDY 6	
	2 RKLVDY 7	

AAW34290
 ID AAW34290 standard; peptide; 7 AA.
 XX
 AC AAW34290;
 XX
 DT 14-MAY-1998 (first entry)
 XX
 DE Human kringle 5 peptide fragment.
 XX
 KW Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
 KW metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
 KW psoriasis; arthritis; macular degeneration; diabetic retinopathy;
 KW autoimmune disease; ocular disease; capillary proliferation; therapy;
 KW kringle 5 receptor.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "optionally has nitrogen protecting group"
 FT Modified-site 7 /note= "3-I-Tyrosyl"
 FT Misc-difference 7 /note= "optionally has carboxylic acid protecting group"
 FT
 XX WO9741824-A2.
 XX
 PD 13-NOV-1997.
 XX
 PF 05-MAY-1997; 97WO-US07700.
 XX
 PR 03-APR-1997; 97US-0832087.
 PR 03-MAY-1996; 96US-0643219.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Davidson DJ, Gubbins EJ, Wang J;
 DR WPI; 1997-558670/51.
 XX
 PT New kringle 5 peptide(s) and fusion proteins derived from
 PT plasminogen - useful as anti-angiogenesis agents for treating
 PT cancer, psoriasis, arthritis etc., including gene therapy
 XX
 PS Claim 62; Page 67; 78pp; English.
 XX
 CC This sequence is a kringle 5 (K5) peptide homologous to human
 CC plasminogen. K5 peptide fragments homologous to this sequence, are
 CC anti-angiogenesis agents, specifically for treating or preventing cancer,
 CC particularly primary or metastatic solid tumours, carcinomas, sarcomas,
 CC lymphomas, haemangiomas. They can also be used for treating or preventing
 CC psoriasis, arthritis, macular degeneration and diabetic retinopathy. The
 CC fragments can also be used to treat autoimmune or ocular diseases;
 CC capillary proliferation within atherosclerotic plaque, haemophilic
 CC joints, wound granulation, ulcers etc., also as contraceptives that
 CC inhibit ovulation and establishment of the placenta. K5 antisera or
 CC (ant)agonists can be used similarly, optionally coupled to cytotoxic
 CC agents. Antagonists may be used to induce angiogenesis, e.g. for wound
 CC healing. The K5 peptides are also used to raise specific antibodies (Ab),
 CC for diagnosis and for affinity purification of K5 receptors. The K5
 CC receptors may then be expressed in tumour cells to increase their
 CC response to the peptides or used for identification of smaller
 CC antagonists. The Ab are used to detect/quantify the peptides in
 CC biological samples. The K5 peptides (and K5 fusion proteins) selectively
 CC inhibit proliferation of endothelial cells with low toxicity against
 CC normal cells. Typically they have 800-times greater inhibitory activity
 CC against bovine capillary cells in vitro than kringle 1-4 peptides.
 XX
 SO Sequence 7 AA;
 Query Match 100.0%; Score 6; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
 DB 2 RKLYDY 7
 RESULT 10
 AAW34291
 ID AAW34291 standard; peptide; 7 AA.
 XX
 AC AAW34291;
 XX
 DT 14-MAY-1998 (first entry)
 XX
 DE Human kringle 5 peptide fragment.
 XX
 KW Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
 KW metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
 KW psoriasis; arthritis; macular degeneration; diabetic retinopathy;
 KW autoimmune disease; ocular disease; capillary proliferation; therapy;
 KW kringle 5 receptor.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "optionally has nitrogen protecting group"
 FT Modified-site 5 /note= "3-I-Tyrosyl"
 FT Misc-difference 7 /note= "optionally has carboxylic acid protecting group"
 FT
 XX WO9741824-A2.
 XX
 PD 13-NOV-1997.
 XX
 PF 05-MAY-1997; 97WO-US07700.
 XX
 PR 03-APR-1997; 97US-0832087.
 PR 03-MAY-1996; 96US-0643219.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Davidson DJ, Gubbins EJ, Wang J;
 DR WPI; 1997-558670/51.
 XX
 PT New kringle 5 peptide(s) and fusion proteins derived from
 PT plasminogen - useful as anti-angiogenesis agents for treating
 PT cancer, psoriasis, arthritis etc., including gene therapy
 XX
 PS Claim 62; Page 67; 78pp; English.
 XX
 CC This sequence is a kringle 5 (K5) peptide homologous to human
 CC plasminogen. K5 peptide fragments homologous to this sequence, are
 CC anti-angiogenesis agents, specifically for treating or preventing cancer,
 CC particularly primary or metastatic solid tumours, carcinomas, sarcomas,
 CC lymphomas, haemangiomas. They can also be used for treating or preventing
 CC psoriasis, arthritis, macular degeneration and diabetic retinopathy. The
 CC fragments can also be used to treat autoimmune or ocular diseases;
 CC capillary proliferation within atherosclerotic plaque, haemophilic
 CC joints, wound granulation, ulcers etc., also as contraceptives that
 CC inhibit ovulation and establishment of the placenta. K5 antisera or
 CC (ant)agonists can be used similarly, optionally coupled to cytotoxic
 CC agents. Antagonists may be used to induce angiogenesis, e.g. for wound
 CC healing. The K5 peptides are also used to raise specific antibodies (Ab),
 CC for diagnosis and for affinity purification of K5 receptors. The K5
 CC receptors may then be expressed in tumour cells to increase their
 CC response to the peptides or used for identification of smaller
 CC antagonists. The Ab are used to detect/quantify the peptides in
 CC biological samples. The K5 peptides (and K5 fusion proteins) selectively
 CC inhibit proliferation of endothelial cells with low toxicity against
 CC normal cells. Typically they have 800-times greater inhibitory activity

CC against bovine capillary cells in vitro than kringle 1-4 peptides.
XX Sequence 7 AA;

Query Match 100.0%; Score 6; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYD 6
| | | | |
Db 2 RKLYD 7

RESULT 11
AAB01888
ID AAB01888 standard; peptide; 7 AA.

AC AAB01888;
DT 18-SEP-2000 (first entry)

XX Human plasminogen kringle 5-derived peptide, SEQ ID NO:6.

XX Plasminogen; human; kringle 5 domain; endothelial cell proliferation;
KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
KW antiproliferative; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
KW antiangiogenic; cancer; tumour; autoimmune disease.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl moiety"
FT Modified-site 5 /note= "3-Iodotyrosine"
FT Modified-site 7 /note= "C-terminal amide moiety"

XX US6057122-A.

XX 02-MAY-2000.

XX 05-MAY-1997; 97US-0851350.

XX 03-MAY-1996; 96US-0643219.

XX 03-APR-1997; 97US-0832087.

XX (ABBO) ABBOTT LAB.

XX Davidson DJ;

XX WPI; 2000-349573/30.

XX Preparation of Kringle five peptide fragment for treating various
XX disorders such as angiogenic, ocular, skin diseases and cancer,
XX involves mixing mammalian plasminogen and elastase followed by
XX incubation and isolation -

XX Example 10; Column 38; 48pp; English.

XX The invention relates to a method of preparing plasminogen kringle 5
XX peptide fragments. The method comprises mixing mammalian plasminogen and
XX elastase in the ratio 1:100-1:300, followed by incubating and isolating
XX the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
XX endothelial cell proliferation and migration. The peptides are useful
XX for treating angiogenic diseases, primary and metastatic solid tumours
XX and carcinomas of various organs such as breast, genital tract,
XX endocrine glands, skin, tumours of the brain and eyes and solid tumours
XX arising from haematopoietic malignancies such as leukaemias and
XX lymphomas. They are also used for the prophylaxis of various autoimmune
XX diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
XX (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber

CC Syndrome), diseases caused by excessive or abnormal stimulation of
CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
CC disease and ulcers). The peptides are also useful as a birth control
CC agent which inhibits ovulation and establishment of the placenta.
CC Sequences AAB01888, AAB01889 and AAB01895-B01905 represent human
CC plasminogen kringle 5-derived peptides synthesised and used in
CC exemplifications of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 6; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLYD 6
| | | | |
Db 2 RKLYD 7

RESULT 12
AAB01889
ID AAB01889 standard; peptide; 7 AA.

AC AAB01889;

DT 18-SEP-2000 (first entry)

XX Human plasminogen kringle 5-derived peptide, SEQ ID NO:18.

XX Plasminogen; human; kringle 5 domain; endothelial cell proliferation;
KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
KW antiproliferative; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
KW antiangiogenic; cancer; tumour; autoimmune disease.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl moiety"
FT Modified-site 7 /note= "3-Iodotyrosine; C-terminal amide moiety"

XX US6057122-A.

XX 02-MAY-2000.

XX 05-MAY-1997; 97US-0851350.

XX 03-MAY-1996; 96US-0643219.

XX 03-APR-1997; 97US-0832087.

XX (ABBO) ABBOTT LAB.

XX Davidson DJ;

XX WPI; 2000-349573/30.

XX Preparation of Kringle five peptide fragment for treating various
XX disorders such as angiogenic, ocular, skin diseases and cancer,
XX involves mixing mammalian plasminogen and elastase followed by
XX incubation and isolation -

XX Example 11; Column 38; 48pp; English.

XX The invention relates to a method of preparing plasminogen kringle 5
XX peptide fragments. The method comprises mixing mammalian plasminogen and
XX elastase in the ratio 1:100-1:300, followed by incubating and isolating
XX the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
XX endothelial cell proliferation and migration. The peptides are useful
XX for treating angiogenic diseases, primary and metastatic solid tumours
XX and carcinomas of various organs such as breast, genital tract,

CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukaemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
 CC syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01888, AAB01889 and AAB01895-B01905 represent human
 CC plasminogen kringle 5-derived peptides synthesised and used in
 CC exemplifications of the invention.

CC Sequence 7 AA:

Query Match 100.0%; Score 6; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
 Db 2 RKLYDY 7

RESULT 13

AAB01900 standard; peptide; 7 AA.

AC AAB01900;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringle 5 peptide fragment #6.

KW Plasminogen; human; kringle 5 domain; endothelial cell proliferation;
 KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
 KW antipsoriatic; antiinflammatory; antitumor; antirheumatic; antiarthritic;
 KW antiangiogenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

Key Location/Qualifiers

FT Modified-site 1

FT Modified-site /note= "N-terminal acetyl moiety"

FT Modified-site 7

/note= "C-terminal amide moiety"

PN US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

PR 03-MAY-1996; 96US-06432219.

PR 03-APR-1997; 97US-0832087.

PA (ABBO) ABBOTT LAB.

PI Davidson DJ;

DR WPI; 2000-349573/30.

PT Preparation of kringle five peptide fragment for treating various
 PT disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -

PS Example 6; Column 36; 48pp; English.

CC The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating

CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukaemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
 CC syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01888, AAB01889 and AAB01895-B01905 represent human
 CC plasminogen kringle 5-derived peptides synthesised and used in
 CC exemplifications of the invention.

CC Sequence 7 AA:

Query Match 100.0%; Score 6; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
 Db 2 RKLYDY 7

RESULT 14

AAB92097 standard; Peptide; 7 AA.

AC AAB92097;

DT 22-JUN-2001 (first entry)

DE Laminin fragment SEQ ID NO:1273.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000MO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT -
 PS Disclosure; Page 612; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB50829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 6; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVDY 6
 |||||
 Db 1 RKLVDY 6

RESULT 15
 AAB36571
 ID AAB36571 standard; Peptide: 7 AA.

XX AC AAB36571;

XX DT 09-MAR-2001 (first entry)

DE Mammalian kringle 5 peptide SEQ ID NO:10.

XX KW Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory;
 KW vasotrophic; cytostatic; antithrombotic; antipsoriatic; antidiabetic;
 KW antiarteriosclerotic; osteoprotic; angiogenesis inhibitor; angiogenesis;
 KW inflammatory disorder; inflammation; chronic articular rheumatism;
 KW psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis;
 KW capillary proliferation; atherosclerotic plaque; osteoporosis;
 KW cancer; solid tumour; angiofibroma; retrolental fibroplasia;
 KW haemangioma; Kasposi's sarcoma; neovascularisation; tumour growth.

XX OS Mammalia.

XX PN WO200070665-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-IB00763.

XX PR 17-MAY-1999; 99US-0134406.

XX PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Rasamoeliso M, Thiabaudeau K, Huang X, Bellevue R;

XX WPI; 2001-090970/10.

XX PT New modified anti-angiogenic kringle 5 peptides capable of forming
 XX conjugates with blood proteins, useful for treating angiogenesis,
 XX inappropriate invasion of vessels or cancers in humans or mammals

XX PS Claim 6; Page 9; 82pp; English.

XX CC The present invention describes a modified anti-angiogenic peptide (I)
 CC comprising a reactive group that reacts with amino groups, hydroxyl
 CC groups or thiol groups on blood components to form stable covalent
 CC bonds. The reactive group is selected from succinimidyl or maleimido
 CC groups. (I) can have anti-inflammatory, vasotrophic, cytostatic,
 CC antithrombotic, antipsoriatic, antidiabetic, antiarteriosclerotic and
 CC osteoprotic activities, and is an angiogenesis inhibitor. (I) are useful
 CC for treating angiogenesis in a human, where the derivative is reacted

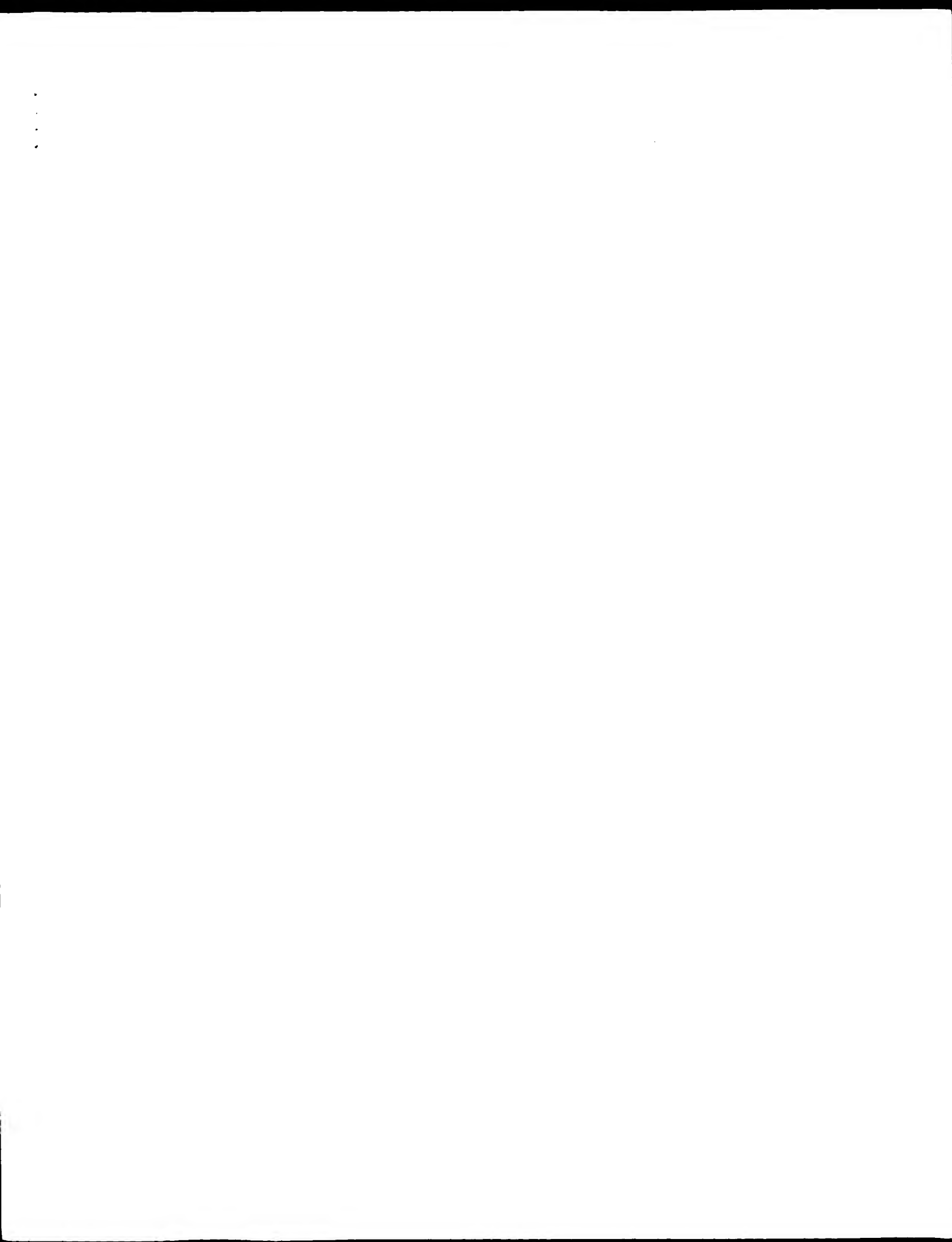
CC with blood proteins. (II) are also useful for manufacturing a medicament
 CC extending the in vivo half-life of a kringle 5 peptide in a patient to
 CC provide an anti-angiogenic effect. In particular, a modified kringle 5
 CC peptide can be used for treating inflammatory disorders (e.g. immune and
 CC non-immune inflammation, chronic articular rheumatism or psoriasis),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis,
 CC capillary proliferation in atherosclerotic plaques or osteoporosis), or
 CC cancer associated disorders (e.g. solid tumours, solid tumour
 CC metastases, angiofibromas, retrolental fibroplasia, haemangiomas,
 CC Kasposi's sarcoma or other cancers requiring neovascularisation to
 CC support tumour growth). The peptides are useful for treating these
 CC diseases in mammalian or human patients. AAB36562 represents a mammalian
 CC kringle 5 protein, and AAB36563 to AAB36577 represent specifically
 CC claimed kringle 5 peptides from the present invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 6; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLVDY 6
 |||||
 Db 1 RKLVDY 6

Search completed: November 8, 2002, 09:37:20
 Job time : 30 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:21 : Search time 17.6667 Seconds

(without alignments)
37.723 Million cell updates/sec

Title: US-09-657-431-11

Perfect score: 34
Sequence: 1 RKLXYD 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	6	18	AAW34302
2	34	100.0	6	21	AAAB01903
3	34	100.0	6	22	AAAB92098
4	34	100.0	6	22	AAAB36572
5	34	100.0	7	18	AAW34303
6	34	100.0	7	18	AAW34304
7	34	100.0	7	18	AAW34306
8	34	100.0	7	18	AAW34299
9	34	100.0	7	18	AAW34290
10	34	100.0	7	18	AAW34291
11	34	100.0	7	21	AAAB01888

12	34	100.0	7	21	AAAB01889
13	34	100.0	7	21	AAAB01900
14	34	100.0	7	22	AAAB92097
15	34	100.0	7	22	AAAB36571
16	34	100.0	7	22	AAAB36576
17	34	100.0	8	22	AAAB3292
18	34	100.0	8	22	AAAB92092
19	34	100.0	8	22	AAAB92101
20	34	100.0	8	22	AAAB36567
21	34	100.0	8	22	AAAB36575
22	34	100.0	11	18	AAW34298
23	34	100.0	11	22	AAAB01889
24	34	100.0	11	22	AAAB92094
25	34	100.0	11	22	AAAB36569
26	34	100.0	12	22	AAAB92089
27	34	100.0	12	22	AAAB92093
28	34	100.0	12	22	AAAB36564
29	34	100.0	12	22	AAAB36568
30	34	100.0	21	21	AAAB15521
31	34	100.0	23	22	AAAB36583
32	34	100.0	23	22	AAAB92096
33	34	100.0	23	22	AAAB36570
34	34	100.0	24	22	AAAB92090
35	34	100.0	24	22	AAAB92095
36	34	100.0	24	22	AAAB36565
37	34	100.0	79	18	AAW19256
38	34	100.0	85	21	AAAB08413
39	34	100.0	90	21	AAAB01914
40	34	100.0	91	21	AAV58868
41	34	100.0	93	21	AAAB01917
42	34	100.0	95	21	AAAB01913
43	34	100.0	98	21	AAAB01916
44	34	100.0	101	18	AAW34286
45	34	100.0	101	21	AAAB01890

ALIGNMENTS

RESULT 1	
AAW34302	standard; peptide; 6 AA.
XX	
AC	AAW34302.
XX	
DT	14-MAY-1998 (first entry)
XX	
DE	Kring 5 peptide fragment.
XX	
KW	Plasminogen; human; Kring 5 peptide; anti-angiogenesis agent; cancer;
KW	metastatic solid tumor; carcinoma; sarcoma; lymphoma; haemangioma;
KW	psoriasis; arthritis; macular degeneration; diabetic retinopathy;
KW	autoimmune disease; ocular disease; capillary proliferation; therapy;
XX	Kring 5 receptor.
OS	Synthetic.
XX	
PH	Key
FT	Modified-site 1 Location/Qualifiers
FT	/note= "N-Ac-Arg"
FT	Modified-site 6 /note= "C-terminal amide"
XX	
PN	WO97A1824-A2.
XX	
PD	13-NOV-1997.
XX	
PF	05-MAY-1997; 97MO-US07700.
XX	
PR	03-APR-1997; 97US-0832087.
XX	
PA	03-MAY-1996; 96US-0643219.
XX	
XX	(ABBO) ABBOTT LAB.

XX Davidson DJ, Gubbins EJ, Wang J;
PI
XX
DR WPI: 1997-558670/51.
XX
XX New kringle 5 peptide(s) and fusion proteins derived from
PT plasminogen - useful as anti-angiogenesis agents for treating
PT cancer, psoriasis, arthritis etc., including gene therapy
XX
PS
Example 9; Page 45; 78pp; English.

Example 9; Page 45; 78pp; English.

This sequence is synthetic a kringle 5 (K5) peptide homologous to human plasminogen K5 peptide fragments homologous to this sequence, are anti-angiogenesis agents, specifically for treating or preventing cancer, particularly primary or metastatic solid tumours, carcinomas, sarcomas, lymphomas, haemangiomas. They can also be used for treating or preventing psoriasis, arthritis, macular degeneration and diabetic retinopathy. The fragments can also be used to treat autoimmune or ocular diseases, capillary proliferation within atherosclerotic plaque, haemophilic joints, wound granulation, ulcers etc., also as contraceptives that inhibit ovulation and establishment of the placenta. K5 antisera or (ant)agonists can be used similarly, optionally coupled to cytotoxic agents. Antagonists may be used to induce angiogenesis, e.g. for wound healing. The K5 peptides are also used to raise specific antibodies (Ab) for diagnosis and for affinity purification of K5 receptors. The K5 receptors may then be expressed in tumour cells to increase their response to the peptides or used for identification of smaller antagonists. The Ab are used to detect/quantify the peptides in biological samples. The K5 peptides (and K5 fusion proteins) selectively inhibit proliferation of endothelial cells with low toxicity against normal cells. Typically they have 800-times greater inhibitory activity against bovine capillary cells *in vitro* than kringle 1-4 peptides.

Sequence 6 AA;

Query Match	100.0%	Score 34	DB 18	length 6
Best Local Similarity	100.0%	Pred. No.	6.4e+05	
Matches	6	Conservative	0	Indels
		Mismatches	0	Gaps

QY	1	RKLYDY	6
		111111	
Db	1	RKLYDY	6

```

RESULT 2
AAB01903
ID AAB01903 standard; peptide; 6 AA

```

AC	AAB01903;
XX	
DT	18-SEP-2000 (first entry)

DE Human plasminogen kringle 5 peptide fragment #9.

KW Plasminogen; human; kringle 5 domain; endothelial cell proliferation;
KW angiogenesis; antiproliferative; antiarteriosclerotic; cytosolic;
KM antipsoriatic; antinflammatory; antitumor; anthrasmatic; antarturic;
KW antillogenic; cancer; tumour; autoimmune disease.
XX
OS Homo sapiens.

Homo sapiens.

FH	Key	Location/Qualifiers
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2	2	2
3	3	3
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97	97	97
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99	99	99
100	100	100

FT	/note= "N-terminal acetyl moiety"
FT	6
FT	/note= "C-terminal amide moiety"

PN US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

XX

PR 03-MAY-1996; 96US-0643219.
PR 03-APR-1997; 97US-0832087.
XX
XX
PA (ABBO) ABBOTT LAB.
XX
PI Davidson DJ;
XX
DR WPI, 2000-349573/30.

WPI; 2000-349573/30.

PT Preparation of Kringling five peptide fragment for treating various
PT disorders such as angiogenic, ocular, skin diseases and cancer,
PT involves mixing mammalian plasminogen and elastase followed by
PT incubation and isolation -

PS Example 9; Column 37; 48pp; English

CC The invention relates to a method of preparing plasminogen kringle 5
CC peptide fragments. The method comprises mixing mammalian plasminogen
CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
CC endothelial cell proliferation and migration. The peptides are useful
CC for treating angiogenic diseases, primary and metastatic solid tumours
CC and carcinomas of various organs such as breast, genital tract,
CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
CC arising from haematopoietic malignancies such as leukaemias and
CC lymphomas. They are also used for the prophylaxis of various autoimmune
CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webb
CC disease), diseases caused by excessive or abnormal stimulation of
CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
CC which have angiogenesis as a pathological consequence (e.g., cat scratch
CC disease and ulcers). The peptides are also useful as a birth control
CC agent which inhibits ovulation and establishment of the placenta.
CC Sequences AA801888, AA801889 and AA801895-801905 represent human
CC plasminogen kringle 5-derived peptides synthesised and used in
CC exemplifications of the invention.

Sequence 6 AA;

Query Match	100.0%;	Score 34;	DB 21;	Length 6;
Best Local Similarity	100.0%;	Pred. No. 6;	4e+05;	
Matches	6;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY	1	RKLYDY	6
Db	1	RKLYDY	6

RESULT 3
AAB92098
ID AAB92098 standard; Peptide; 6 AA

AC AAB92098;

DT 22-JUN-2001 (first entry)

DE Laminin fragment SEQ ID NO:1274.

KM protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

hydroxyl; thi

OS Homo sapiens.

XX

XX
3
3
4
3
3
3

XX
XX

XX 17 MAY 1000 - 00175-0134406

PR 10-SEP-1999; 99US-0153406.

[illegible]

FT	/note= "N-Ac-Pro"
FT	Modified-site 7
FT	/note= "3-I-tyrosyl"
FT	Modified-site 7
XX	/note= "C-terminal amide"
XX	
PX	WO9741824-A2.
PN	
PD	13-NOV-1997.
XX	
PF	05-MAY-1997; 97WO-US07700.
XX	
PR	03-APR-1997; 97US-0832087.
PR	03-MAY-1996; 96US-0643219.
XX	
PA	(ABBO) ABBOTT LAB.
PI	
PI	Davidson DJ, Gubbins EJ, Wang J;
DR	WPI; 1997-558670/51.
XX	
PT	New Kringle 5 peptide(s) and fusion proteins derived from
PT	Plasminogen - useful as anti-angiogenesis agents for treating
PT	cancer, psoriasis, arthritis etc., including gene therapy
PS	
PS	Example 11; Page 45; 78pp: English.
XX	
CC	This sequence is synthetic a kringle 5 (K5) peptide homologous to human
CC	plasminogen. K5 peptide fragments homologous to this sequence, are
CC	anti-angiogenesis agents, specifically for treating or preventing cancer,
CC	particularly primary or metastatic solid tumours, carcinomas, sarcomas,
CC	lymphomas, haemangiomas. They can also be used for treating or preventing
CC	psoriasis, arthritis, macular degeneration and diabetic retinopathy. The
CC	fragments can also be used to treat autoimmune or ocular diseases,
CC	capillary proliferation within atherosclerotic plaque, haemophilic
CC	joints, wound granulation, ulcers etc., also as contraceptives that
CC	inhibit ovulation and establishment of the placenta. K5 antiserum or
CC	(ant)agonists can be used similarly, optionally coupled to cytotoxic
CC	agents. Antagonists may be used to induce angiogenesis, e.g. for wound
CC	healing. The K5 peptides are also used to raise specific antibodies (Ab),
CC	for diagnosis and for affinity purification of K5 receptors. The K5
CC	receptors may then be expressed in tumour cells to increase their
CC	response to the peptides or used for identification of smaller
CC	antagonists. The Ab are used to detect/quantify the peptides in
CC	biological samples. The K5 peptides (and K5 fusion proteins) selectively
CC	inhibit proliferation of endothelial cells with low toxicity against
CC	normal cells. Typically they have 800-times greater inhibitory activity
CC	against bovine capillary cells in vitro than kringle 1-4 peptides.
XX	
SQ	Sequence 7 AA;
	Query Match 100.0%; Score 34; DB 18; Length 7;
	Best Local Similarity 100.0%; Pred. No. 6.4e+05;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 RKLVDY 6
DB	2 RKLVDY 7
RESULT 7	
AAMW34306	ID AAW34306 standard; peptide; 7 AA.
XX	
AC	AAW34306;
XX	
DT	14-MAY-1998 (first entry)
XX	
DE	Kringle 5 peptide fragment.
XX	
KW	Plasminogen: human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
KW	metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
KW	psoriasis; arthritis; macular degeneration; diabetic retinopathy;

AAW34290
 ID AAW34290 standard; peptide; 7 AA.
 AC AAW34290;
 XX
 DT 14-MAY-1998 (first entry)
 XX
 DE Human kringle 5 peptide fragment.
 DE
 KW Plasmalogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
 KW metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
 KW psoriasis; arthritis; macular degeneration; diabetic retinopathy;
 KW autoimmune disease; ocular disease; capillary proliferation; therapy;
 KW kringle 5 receptor.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "optionally has nitrogen protecting group"
 FT Modified-site 7 /note= "3-I-Tyrosyl"
 FT Misc-difference 7 /note= "optionally has carboxylic acid protecting group"
 FT
 XX
 PN W09741824-A2.
 XX
 PD 13-NOV-1997.
 XX
 PF 05-MAY-1997; 97WO-US07700.
 XX
 PR 03-APR-1997; 97US-0832087.
 PR 03-MAY-1996; 96US-0643219.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Davidson DJ, Gubbins EJ, Wang J;
 XX
 DR WPI; 1997-558670/51.
 XX
 PT New kringle 5 peptide(s) and fusion proteins derived from
 PT plasmalogen - useful as anti-angiogenesis agents for treating
 PT cancer, psoriasis, arthritis etc., including gene therapy
 XX
 PS Claim 62; Page 67; 78pp; English.
 XX
 CC This sequence is a kringle 5 (K5) peptide homologous to human
 CC plasmalogen. K5 peptide fragments homologous to this sequence, are
 CC anti-angiogenesis agents, specifically for treating or preventing cancer,
 CC particularly primary or metastatic solid tumours, carcinomas, sarcomas,
 CC lymphomas, haemangiomas. They can also be used for treating or preventing
 CC psoriasis, arthritis, macular degeneration and diabetic retinopathy. The
 CC fragments can also be used to treat autoimmune or ocular diseases,
 CC capillary proliferation within atherosclerotic plaque, haemophilic
 CC joints, wound granulation, ulcers etc., also as contraceptives that
 CC inhibit ovulation and establishment of the placenta. K5 antisera or
 CC (ant)agonists can be used similarly, optionally coupled to cytotoxic
 CC agents. Antagonists may be used to induce angiogenesis, e.g. for wound
 CC healing. The K5 peptides are also used to raise specific antibodies (Ab),
 CC for diagnosis and for affinity purification of K5 receptors. The K5
 CC receptors may then be expressed in tumour cells to increase their
 CC response to the peptides or used for identification of smaller
 CC antagonists. The Ab are used to detect/quantify the peptides in
 CC biological samples. The K5 peptides (and K5 fusion proteins) selectively
 CC inhibit proliferation of endothelial cells with low toxicity against
 CC normal cells. Typically they have 800-times greater inhibitory activity
 CC against bovine capillary cells in vitro than kringle 1-4 peptides.
 XX
 SO Sequence 7 AA:
 Query Match 100.0%; Score 34; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKLTY 6
 DB 2 RKLTY 7
 RESULT 10
 ID AAW34291 standard; peptide; 7 AA.
 AC AAW34291;
 XX
 DT 14-MAY-1998 (first entry)
 XX
 DE Human kringle 5 peptide fragment.
 DE
 KW Plasmalogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
 KW metastatic solid tumour; carcinoma; sarcoma; lymphoma; haemangioma;
 KW psoriasis; arthritis; macular degeneration; diabetic retinopathy;
 KW autoimmune disease; ocular disease; capillary proliferation; therapy;
 KW kringle 5 receptor.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "optionally has nitrogen protecting group"
 FT Modified-site 5 /note= "3-I-Tyrosyl"
 FT Misc-difference 7 /note= "optionally has carboxylic acid protecting group"
 FT
 XX
 PN W09741824-A2.
 XX
 PD 13-NOV-1997.
 XX
 PF 05-MAY-1997; 97WO-US07700.
 XX
 PR 03-APR-1997; 97US-0832087.
 PR 03-MAY-1996; 96US-0643219.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Davidson DJ, Gubbins EJ, Wang J;
 XX
 DR WPI; 1997-558670/51.
 XX
 PT New kringle 5 peptide(s) and fusion proteins derived from
 PT plasmalogen - useful as anti-angiogenesis agents for treating
 PT cancer, psoriasis, arthritis etc., including gene therapy
 XX
 PS Claim 62; Page 67; 78pp; English.
 XX
 CC This sequence is a kringle 5 (K5) peptide homologous to human
 CC plasmalogen. K5 peptide fragments homologous to this sequence, are
 CC anti-angiogenesis agents, specifically for treating or preventing cancer,
 CC particularly primary or metastatic solid tumours, carcinomas, sarcomas,
 CC lymphomas, haemangiomas. They can also be used for treating or preventing
 CC psoriasis, arthritis, macular degeneration and diabetic retinopathy. The
 CC fragments can also be used to treat autoimmune or ocular diseases,
 CC capillary proliferation within atherosclerotic plaque, haemophilic
 CC joints, wound granulation, ulcers etc., also as contraceptives that
 CC inhibit ovulation and establishment of the placenta. K5 antisera or
 CC (ant)agonists can be used similarly, optionally coupled to cytotoxic
 CC agents. Antagonists may be used to induce angiogenesis, e.g. for wound
 CC healing. The K5 peptides are also used to raise specific antibodies (Ab),
 CC for diagnosis and for affinity purification of K5 receptors. The K5
 CC receptors may then be expressed in tumour cells to increase their
 CC response to the peptides or used for identification of smaller
 CC antagonists. The Ab are used to detect/quantify the peptides in
 CC biological samples. The K5 peptides (and K5 fusion proteins) selectively
 CC inhibit proliferation of endothelial cells with low toxicity against
 CC normal cells. Typically they have 800-times greater inhibitory activity

CC against bovine capillary cells in vitro than kringle 1-4 peptides.
XX
SQ Sequence 7 AA:

Query Match 100.0%; Score 34; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
|||||
DB 2 RKLYDY 7

RESULT 11
AAB01888
ID AAB01888 standard; peptide; 7 AA.
XX
AC AAB01888;
XX
DT 18-SEP-2000 (first entry)

Human plasminogen kringle 5-derived peptide, SEQ ID NO:6.

XX Plasminogen; human; kringle 5 domain; endothelial cell proliferation;
KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
KW antiproliferative; antiinflammatory; antitumor; antineoplastic; antitumor;
KW antitumor; cancer; tumor; autoimmune disease.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl moiety"

FT Modified-site 5 /note= "3-Iodotyrosine"

FT Modified-site 7 /note= "C-terminal amide moiety"

XX US6057122-A.

XX 02-MAY-2000.

XX 05-MAY-1997; 97US-0851350.

XX 03-MAY-1996; 96US-0643219.

XX 03-APR-1997; 97US-0832087.

XX (ABBO) ABBOTT LAB.

XX Davidson DJ;

XX WPI; 2000-349573/30.

XX Preparation of Kringle five peptide fragment for treating various
XX disorders such as angiogenic, ocular, skin diseases and cancer,
XX involves mixing mammalian plasminogen and elastase followed by
XX incubation and isolation -

XX Example 10; Column 38; 48pp; English.

XX The invention relates to a method of preparing plasminogen kringle 5
XX peptide fragments. The method comprises mixing mammalian plasminogen and
XX elastase in the ratio 1:100-1:300, followed by incubating and isolating
XX the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
XX endothelial cell proliferation and migration. The peptides are useful
XX for treating angiogenic diseases, primary and metastatic solid tumours
XX and carcinomas of various organs such as breast, genital tract,
XX endocrine glands, skin, tumours of the brain and eyes and solid tumours
XX arising from haematopoietic malignancies such as leukaemias and
XX lymphomas. They are also used for the prophylaxis of various autoimmune
XX diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
XX (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber

CC Syndrome), diseases caused by excessive or abnormal stimulation of
CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
CC disease and ulcers). The peptides are also useful as a birth control
CC agent which inhibits ovulation and establishment of the placenta.
CC Sequences AAB01888, AAB01889 and AAB01895-B01905 represent human
CC plasminogen kringle 5-derived peptide synthetised and used in
CC exemplifications of the invention.

SQ Sequence 7 AA:

Query Match 100.0%; Score 34; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
|||||
DB 2 RKLYDY 7

RESULT 12
AAB01889
ID AAB01889 standard; peptide; 7 AA.
XX
AC AAB01889;
XX
DT 18-SEP-2000 (first entry)

Human plasminogen kringle 5-derived peptide, SEQ ID NO:18.

XX Plasminogen; human; kringle 5 domain; endothelial cell proliferation;
KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
KW antiproliferative; antiinflammatory; antitumor; antineoplastic; antitumor;
KW antitumor; cancer; tumor; autoimmune disease.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl moiety"

FT Modified-site 7 /note= "3-Iodotyrosine; C-terminal amide moiety"

XX US6057122-A.

XX 02-MAY-2000.

XX 05-MAY-1997; 97US-0851350.

XX 03-MAY-1996; 96US-0643219.

XX 03-APR-1997; 97US-0832087.

XX (ABBO) ABBOTT LAB.

XX Davidson DJ;

XX WPI; 2000-349573/30.

XX Preparation of Kringle five peptide fragment for treating various
XX disorders such as angiogenic, ocular, skin diseases and cancer,
XX involves mixing mammalian plasminogen and elastase followed by
XX incubation and isolation -

XX Example 11; Column 38; 48pp; English.

XX The invention relates to a method of preparing plasminogen kringle 5
XX peptide fragments. The method comprises mixing mammalian plasminogen and
XX elastase in the ratio 1:100-1:300, followed by incubating and isolating
XX the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
XX endothelial cell proliferation and migration. The peptides are useful
XX for treating angiogenic diseases, primary and metastatic solid tumours
XX and carcinomas of various organs such as breast, genital tract,

CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
 CC Syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01888, AAB01889 and AAB01895-B01905 represent human
 CC plasminogen kringle 5-derived peptides synthesised and used in
 CC exemplifications of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
 |||||
 Db 2 RKLYDY 7

RESULT 13

ID AAB01900 standard; peptide; 7 AA.

XX AAB01900;

DT 18-SEP-2000 (first entry)

XX Human plasminogen kringle 5 peptide fragment #6.

XX Plasminogen; human; kringle 5 domain; endothelial cell proliferation;

KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;

KM antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic;

XX antitumorigenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

XX Key

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
 CC Syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01888, AAB01889 and AAB01895-B01905 represent human
 CC plasminogen kringle 5-derived peptides synthesised and used in
 CC exemplifications of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
 |||||
 Db 2 RKLYDY 7

RESULT 14

ID AAB92097 standard; Peptide; 7 AA.

XX AAB92097;

DT 22-JUN-2001 (first entry)

XX Laminin fragment SpQ ID NO:1273.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;

KW blood component; modification; succinimide; maleimido group; amino;

XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

XX Synthetic.

XX WO20069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents

XX peptidase degradation, useful for increasing length of in vivo activity

XX Disclosure; Page 612; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)

XX comprising a therapeutically active amino acid region (III) and a

XX reactive group (II) (e.g. succinimide and maleimido groups) attached to

XX a less therapeutically active amino acid region (IV), which covalently

XX bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (1) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX SQ Sequence 7 AA;
 CC Query Match 100.0%; Score 34; DB 22; Length 7;
 CC Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
 CC | | | | |
 DB 1 RKLYDY 6

RESULT 15
 AAB36571
 ID AAB36571 standard; Peptide; 7 AA.
 AC AAB36571;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Mammalian kringle 5 peptide SEQ ID NO:10.
 XX
 KW Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory;
 KW vasotropic; cytostatic; antirheumatic; antipruritic; antidiabetic;
 KW antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogenesis;
 KW inflammatory disorder; inflammation; chronic articular rheumatism;
 KW psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis;
 KW capillary proliferation; atherosclerotic plaque; osteoporosis;
 KW cancer; solid tumour; angiofibroma; retrolental fibroplasia;
 KW haemangioma; Kasposi's sarcoma; neovascularisation; tumour growth.
 XX
 OS Mammalia.
 XX
 PN WO20070665-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-IB00763.
 XX
 PR 17-MAY-1999; 99US-0134406.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Rasamoeliso M, Thibaudau K, Huang X, Beliveau R;
 XX WPI; 2001-090970/10.
 DR
 XX
 PT New modified anti-angiogenic kringle 5 peptides capable of forming
 PT conjugates with blood proteins, useful for treating angiogenesis;
 PT inappropriate invasion of vessels or cancers in humans or mammals
 XX
 PS Claim 6; Page 9; 82pp; English.
 XX
 CC The present invention describes a modified anti-angiogenic peptide (1)
 CC comprising a reactive group that reacts with amino groups, hydroxyl
 CC groups or thiol groups on blood components to form stable covalent
 CC bonds. The reactive group is selected from succinimidyl or maleimido
 CC groups (1) can have anti-inflammatory, vasotropic, cytostatic,
 CC antirheumatic, antipruritic, antidiabetic, antiarteriosclerotic and
 CC osteopathic activities, and is an angiogenesis inhibitor. (1) are useful
 CC for treating angiogenesis in a human, where the derivative is reacted

CC with blood proteins. (1) are also useful for manufacturing a medicament
 CC extending the in vivo half-life of a kringle 5 peptide in a patient to
 CC provide an anti-angiogenic effect. In particular, a modified kringle 5
 CC peptide can be used for treating inflammatory disorders (e.g. immune and
 CC non-immune inflammation, chronic articular rheumatism or psoriasis),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis,
 CC capillary proliferation in atherosclerotic plaques or osteoporosis), or
 CC cancer associated disorders (e.g. solid tumours, solid tumour
 CC metastases, angiofibromas, retrolental fibroplasia, haemangiomas,
 CC Kasposi's sarcoma or other cancers requiring neovascularisation to
 CC support tumour growth). The peptides are useful for treating these
 CC diseases in mammalian or human patients. AAB36562 represents a mammalian
 CC kringle 5 protein, and AAB36563 to AAB36577 represent specifically
 CC claimed kringle 5 peptides from the present invention.

XX SQ Sequence 7 AA;
 CC Query Match 100.0%; Score 34; DB 22; Length 7;
 CC Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKLYDY 6
 CC | | | | |
 DB 1 RKLYDY 6

Search completed: November 8, 2002, 09:34:52
 Job time : 18.6667 secs

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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:22 : Search time 28.6667 Seconds
(Without alignments)
72.416 Million cell updates/sec

Title: US-09-657-431-5
Perfect score: 75
Sequence: 1 RNPBGDYGPMK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17294929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	93.3	334	6 O46507	O46507 papio hamad
2	70	93.3	810	4 O15146	O15146 homo sapien
3	64	85.3	567	4 O13208	O13208 homo sapien
4	64	85.3	648	4 O9H1V4	O9H1V4 homo sapien
5	64	85.3	812	11 O9R0W3	O9R0W3 rattus norv
6	64	85.3	812	11 O91WJ5	O91WJ5 mus musculu
7	58	77.3	806	6 O18783	O18783 macropus eu
8	56	74.7	716	11 P70521	P70521 rattus norv
9	56	74.7	716	11 O91XG8	O91XG8 mus musculu
10	55	73.3	709	13 O90ZM6	O90ZM6 brachydanio
11	53	70.7	710	13 O91402	O91402 xenopus. he
12	52	69.3	75	6 O9BGN9	O9BGN9 bos taurus
13	52	69.3	109	6 O9M1B8	O9M1B8 ovis aries
14	52	69.3	208	4 O9B7M0	O9B7M0 homo sapien
15	52	69.3	210	4 O13494	O13494 homo sapien
16	52	69.3	211	11 O55027	O55027 mus musculu

17	52	69.3	290	4 O02935	O02935 homo sapien
18	52	69.3	296	4 O14519	O14519 homo sapien
19	52	69.3	726	13 O90978	O90978 gallus gall
20	52	69.3	728	6 O9B809	O9B809 felis silve
21	50	66.7	111	6 O77688	O77688 onychomys
22	50	66.7	313	13 O9P078	O9P078 crocodylus
23	50	66.7	704	13 O90865	O90865 gallus gall
24	50	66.7	716	13 O91691	O91691 xenopus lae
25	49	65.3	215	13 O42341	O42341 gallus gall
26	48	64.0	263	4 O00318	O00318 homo sapien
27	48	64.0	263	4 O96PE7	O96PE7 homo sapien
28	48	64.0	717	13 P70006	P70006 xenopus lae
29	47.5	63.3	117	4 O9UGS5	O9UGS5 homo sapien
30	47.5	63.3	452	13 O90Y90	O90Y90 xenopus lae
31	47.5	63.3	473	4 O9BY70	O9BY70 homo sapien
32	47.5	63.3	473	11 O99NA3	O99NA3 mus musculu
33	47.5	63.3	473	11 O92454	O92454 rattus norv
34	47.5	63.3	492	4 O96M08	O96M08 homo sapien
35	47	62.7	382	13 O90MT4	O90MT4 crocodylus
36	47	62.7	385	5 O25101	O25101 herdamania m
37	47	62.7	420	13 O90504	O90504 eptaretus
38	46	61.3	260	16 O57371	O57371 borellia bu
39	46	61.3	312	4 O9NSV1	O9NSV1 homo sapien
40	45.5	60.7	399	4 O96GL8	O96GL8 homo sapien
41	45.5	60.7	420	4 O9BTP9	O9BTP9 homo sapien
42	45	60.0	140	11 O9D874	O9D874 mus musculu
43	45	60.0	607	13 O91001	O91001 gallus gall
44	45	60.0	608	13 O9PTW7	O9PTW7 struthio ca
45	44	58.7	522	10 O9L1W0	O9L1W0 oryza sativ

ALIGNMENTS

RESULT 1
ID O46507 PRELIMINARY: PRT: 334 AA.
AC O46507;
DC 01-JUN-1998 (TREMBL:rel. 06, Created)
DT 01-JUN-1998 (TREMBL:rel. 06, Last sequence update)
DE 01-DEC-2001 (TREMBL:rel. 19, Last annotation update)
DE PLASMINOGEN (FRAGMENT).
GN BAPPEP3.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Cox L.A., Jett C., Hixson J.E.;
RT Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice Site Mutation Is Associated with Deletion of a Single Exon in a Null Allele."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY
CC EMBL: AF029692; AB97887.1; -
CC HSSP: P00747; SHP.
CC MEROPS: S01.233; -
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR001254; Trypsin.
CC Pfam: PF00051; Kringle_1.
CC Pfam: PF00089; Trypsin_1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00018; KRINGLE.
CC SMART: SM00020; TRYP_SPC: 1.
CC SMART: SM00021; KRINGLE_1; 1.
CC PROSITE: PS00070; KRINGLE_2; 1.
CC PROSITE: PS50240; TRYPSIN_DOM; 1.
CC PROSITE: PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease.
 FT NON_TER
 SO SEQUENCE 334 AA; 36791 MW; C7DC0E03B965286 CRC64;

Query Match 93.3%; Score 70; DB 6; Length 334;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNPDGVDGCPW 11
 Db 56 RNPDGVDGCPW 66

RESULT 2
 015146 PRELIMINARY; PRT; 810 AA.
 AC 015146;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PLASMINOGEN PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
 RA Mitchell D., Robinson J.H.;
 RT "Expression of recombinant human plasminogen and aglycoplasminogen in
 RT HeLa cells."
 RL Fibrinolysis 0:0-0(1991).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPsin FAMILY.
 DR EMBL; M74220; AAA6451.1; -.
 DR HSSP; P00747; 2PK4.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS50070; KRINGLE_2; 5.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Signal.
 FT SIGNAL 1
 FT CHAIN 20 810 POTENTIAL.
 FT SIGNAL 19 PLASMINOGEN.
 SO SEQUENCE 810 AA; 90555 MW; B05C7D4B0D020B3C CRC64;

Query Match 93.3%; Score 70; DB 4; Length 810;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNPDGVDGCPW 11
 Db 532 RNPDGVDGCPW 542

RESULT 3
 013208
 AC 013208;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN HOMOLOG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20191171; PubMed-10728827;
 RA Degen S.J.F., McDowell S.A., Waltz S.E., Gould F., Stuart L.A.,
 RA Carritt B.;
 RT "Structure of the human DIF151A locus: a chromosome 1 locus with 97%
 RT identity to the chromosome 3 gene coding for hepatocyte growth factor-
 RT like protein."
 RL DNA Seq. 8:409-413(1998).
 DR EMBL; U28054; AAC63092.1; -.
 DR HSSP; P00747; 2PK4.
 DR MEROPS; S01.977; -.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam; PF00051; Kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS50070; KRINGLE_2; 4.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 KW Hydrolyase; Serine protease.
 SO SEQUENCE 567 AA; 64117 MW; 3FC38B07F1645810 CRC64;

Query Match 85.3%; Score 64; DB 4; Length 567;
 Best Local Similarity 90.9%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNPDGVDGCPW 11
 Db 133 RNPDGVDGCPW 143

RESULT 4
 09H1V4 PRELIMINARY; PRT; 648 AA.
 ID 09H1V4;
 AC 09H1V4;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE D1182A14.3 (SIMILAR TO MST1 (MACROPHAGE STIMULATING 1 (HEPATOCYTE
 DE GROWTH FACTOR-LIKE))).
 GN D1182A14.3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bird C.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC EMBL; AL137798; CAC17639.1; -.
 DR HSSP; P00747; 5HPG.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.

RESULT 3
 013208

DR	InterPro:	IPR001254;	Trypstin.
DR	Pfam:	PF000051;	Kringleg_4.
DR	Pfam:	PF000024;	PAN; 1.
DR	Pfam:	PF000089;	Trypsin; 1.
DR	PRINTS:	PR00722;	CHYMOTRYPSIN.
DR	PRINTS:	PRO0018;	KRINGLE.
DR	SMART:	SM00130;	KR; 4.
DR	SMART:	SM00473;	PAN_AP; 1.
DR	SMART:	SM00020;	Tryp_Spc; 1.
DR	PROSITE:	PS00021;	KRINGLE_1; 1.
DR	PROSITE:	PS50070;	KRINGLE_2; 4.
DR	PROSITE:	PS50240;	TRYPsin_DOM; 1.
KW	Hydrolase:	Serine protease.	
SO	SEQUENCE	648 AA; 72781 MW; 4CE077057350E463 CRC64;	
QY	1 RNPDGDVGPGW 11		
Db	113 RNPDGDGPGW 123		
RESULT 5			
ID	Q9ROW3	PRELIMINARY;	PRT; 812 AA.
AC	Q9ROW3;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	PLASMINOGEN PROTEIN PRECURSOR (EC 3.4.21.7).		
GN	PLASMINOGEN.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LIVER;		
RA	Bangert K., Johnsen A.H., Thorsen S.;		
RT	"Rat plasminogen: cDNA and gene structure."		
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LIVER;		
FX	MEDLINE=91250378; PubMed=1645711;		
RA	Kanalas J.J., Makker S.P.;		
RT	"Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor site for plasminogen.";		
RT	J. Biol. Chem. 266:10825-10829(1991).		
CC	-1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.		
CC	EMBL: AJ242649; CAB46014.1; -.		
DR	HSSP: P00747; IPMK.		
DR	MEROPS: S01.233; -.		
DR	InterPro: IPR001314; Chymotrypsin.		
DR	InterPro: IPR000001; Kringleg.		
DR	InterPro: IPR003014; PAN.		
DR	InterPro: IPR003609; Pan_app.		
DR	InterPro: IPR001400; SOMATOSTROPIN.		
DR	InterPro: IPR001254; Trypsin.		
DR	Pfam: PF000051; kringleg_5.		
DR	Pfam: PF000024; PAN; 1.		
DR	Pfam: PF000089; trypsin; 1.		
DR	PRINTS: PR00722; CHYMOTRYPSIN.		
DR	PRINTS: PRO0018; KRINGLE.		
DR	SMART: SM00130; KR; 4.		
DR	SMART: SM00473; PAN_AP; 1.		
DR	SMART: SM00020; Tryp_Spc; 1.		
DR	PROSITE: PS00021; KRINGLE_1; 5.		
DR	PROSITE: PS50070; KRINGLE_2; 5.		
DR	PROSITE: PS00336; SOMATOSTROPIN_2; UNKNOWN_1.		

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DR PROSITE: PS50240; TRYPsin_DOM: 1
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER: 1.
KW Hydrolase; Serine protease; Signal.
FT SIGNAL 1 19
FT CHAIN 20 812 PLASminogen.
SQ SEQUENCE 812 AA; 90535 MW; 8C703C51410EBC9E CRC64;

Query Match 85.3%; Score 64; DB 11; Length 812;
Best Local Similarity 90.9%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDGVDGCPW 11
|||||
Db 532 RNPDGVDNGPW 542

RESULT 6
Q91WJ5 PRELIMINARY; PRT; 812 AA.
AC Q91WJ5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PLASminogen.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC014773; AAH14773.1;
SQ SEQUENCE 812 AA; 90781 MW; 2A173260E6A2FFD2 CRC64;

Query Match 85.3%; Score 64; DB 11; Length 812;
Best Local Similarity 90.9%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDGVDGCPW 11
|||||
Db 532 RNPDGVDNGPW 542

RESULT 7
018783 PRELIMINARY; PRT; 806 AA.
ID 018783;
AC 018783;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PLASminogen.
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98004511; PubMed=9342350;
RA Lahn R.M., Schwartz R., Patchy L.;
RT "Convergent evolution of apolipoprotein(a) in primates and hedgehog.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
CC -; SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC -; TRYPsin FAMILY.
CC EMBL; AF012297; AAB65760.1;
CC HSSP; P00747; 5HP.
DR MEROPS; S01.233;
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.

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DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; kringle_5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 4.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS50070; KRINGLE_2; 5.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR Hydrolase: Serine protease.
 SQ SEQUENCE 806 AA; 90981 MW; 95FAA86DC20064D5 CRC64;

Query Match 77.3%; Score 58; DB 6; Length 806;
 Best Local Similarity 81.8%; Pred. No. 0.42;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNPDGVDGPGW 11
 ||||| |||
 DB 527 RNPDGDHNGPW 537

RESULT 8

P70521 PRELIMINARY; PRT; 716 AA.
 AC P70521.
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MACROPHAGE STIMULATING PROTEIN PRECURSOR.
 GN MSP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=97011126; PubMed=8858136;
 RA Ohshiro K., Iwama A., Matsuno K., Ezaki T., Sakamoto O., Hamaguchi I.,
 RA Takasu N., Suda T.;
 RT "Molecular cloning of Rat Macrophage-stimulating protein and its
 RT involvement in the Male Reproductive System";
 RL Biochem. Biophys. Res. Commun. 227:273-280(1996)
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPsin FAMILY.
 DR EMBL: X95096; CAA64473.1; -.
 DR HSSP: P00747; IKNR.
 DR MEROPS: S01.975; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; kringle_5; 4.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 4.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS50070; KRINGLE_2; 5.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 KW Hydrolase; serine protease; signal.
 FT SIGNAL 1 31 POTENTIAL.
 SQ SEQUENCE 716 AA; 80733 MW; 06B7DF3BF56D921F CRC64;

Query Match 74.7%; Score 56; DB 11; Length 716;
 Best Local Similarity 81.8%; Pred. No. 0.78;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNPDGVDGPGW 11
 ||||| |||
 DB 429 RNPDGDHNGPW 439

RESULT 9

ID 091XG8 PRELIMINARY; PRT; 716 AA.
 AC 091XG8.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HEPATOCYTE GROWTH FACTOR-LIKE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC010551; AAH10551.1; -.
 SQ SEQUENCE 716 AA; 80693 MW; 12474C48A7D4B46D CRC64;

Query Match 74.7%; Score 56; DB 11; Length 716;
 Best Local Similarity 81.8%; Pred. No. 0.78;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNPDGVDGPGW 11
 ||||| |||
 DB 429 RNPDGDHNGPW 439

RESULT 10

ID 090ZNG PRELIMINARY; PRT; 709 AA.
 AC 090ZNG.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HEPATOCYTE GROWTH FACTOR-LIKE 1.
 GN HGF1.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Bassett D.L., Wilson S.W.;
 RT "Early expression of zebrafish Hepatocyte Growth Factor-Like 1
 RT suggests a conserved role in vertebrate neural induction";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF370035; AAK54207.1; -.
 SQ SEQUENCE 709 AA; 81271 MW; 9907236C5DB73A20 CRC64;

Query Match 73.3%; Score 55; DB 13; Length 709;
 Best Local Similarity 81.8%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNPDGVDGPGW 11
 ||||| |||
 DB 422 RNPDGDHNGPW 432

RESULT 11

OY 1 RNPDGVDGPGW 11
 ||||| |||
 DB 422 RNPDGDHNGPW 432


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ID 091402 PRELIMINARY; PRT; 710 AA.
AC 091402;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR.
GN HGF.
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xeropodidae.
OC NCBI_TaxID=8353;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TAILBUD;
RX MEDLINE=95267690; PubMed=7748783;
RA Nakamura H., Tashiro K., Nakamura T., Shiohara K.;
RT "Molecular cloning of Xenopus HGF cDNA and its expression studies in
RL Mech. Dev. 49:123-131(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRIPSIN FAMILY.
DR EMBL; S77422; AAB34354.2; -.
DR HSSP; P14210; 1BHT.
DR MEROPS; S01.976; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Trypsin.
DR Pfam; PF00051; Kringle_4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; Chymotrypsin.
DR PRINTS; PR00018; KRINGLE.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR PROSITE; PS00020; TRYSP; 1.
DR PROSITE; PS00021; KRINGLE_1; 3.
DR PROSITE; PS00070; KRINGLE_2; 4.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
KW Hydrolyase; Serine protease.
SQ SEQUENCE 710 AA; 81487 MW; 5FE6480BE31C27FC CRC64;

Query Match
Best Local Similarity 70.7%; Score 53; DB 13; Length 710;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNPdGVGgPW 11
DB 165 RNPdGVGgPW 175

RESULT 12
ID 09BGN9 PRELIMINARY; PRT; 75 AA.
AC 09BGN9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR (FRAGMENT).
GN HGF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RX Murakami S., Fujiwara C., Miyamoto Y., Takeuchi S., Takahashi S.,
RA Okuda K.;
RT "Expression and action of hepatocyte growth factor in bovine

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RT endometrial stromal and epithelial cells in vitro.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB056447; BAB33031.1; -.
DR HSSP; P14210; 1BHT.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003666; Prothrombin.
DR PRINTS; PR01505; PROTHROMBIN.
DR SMART; SM00130; KR; 2.
DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_1.
DR PROSITE; PS50070; KRINGLE_2; 2.
FT NON_TER 1 75
FT NON_TER 1 75
SQ SEQUENCE 75 AA; 8831 MW; 829EEFCC49701B1 CRC64;

Query Match
Best Local Similarity 69.3%; Score 52; DB 6; Length 75;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNPdGVGgPW 11
DB 4 RNPdGVGgPW 14

RESULT 13
ID 09N1B8 PRELIMINARY; PRT; 109 AA.
AC 09N1B8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR (FRAGMENT).
GN HGF.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM FROM DAY 1 CYCLIC UTERUS;
RX MEDLINE=20297031; PubMed=10819791;
RA Chen C., Spencer T.E., Bazer F.W.;
RT "Expression of hepatocyte growth factor and its receptor c-met in the
RL Biol. Reprod. 62:1844-1850(2000).
DR EMBL; AF213387; AAF25945.1; -.
DR HSSP; P14210; 2HGF.
DR InterPro: IPR000001; Kringle.
DR PRINTS; PR00018; KRINGLE.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
FT NON_TER 1 109
FT NON_TER 1 109
SQ SEQUENCE 109 AA; 12501 MW; 1F88FE5DBC0D4A5D CRC64;

Query Match
Best Local Similarity 69.3%; Score 52; DB 6; Length 109;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNPdGVGgPW 11
DB 67 RNPdGVGgPW 77

RESULT 14
ID 09BYW0 PRELIMINARY; PRT; 208 AA.
AC 09BYW0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

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DE HEPATOCYTE GROWTH FACTOR (FRAGMENT).
GN HGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9136928; PubMed-1832556;
RA Miyazawa K., Kitamura A., Kitamura N.;
RT "Structural organization and the transcription initiation site of the
RL human hepatocyte growth factor gene.";
RL Biochemistry 30:9170-9176(1991).
DR EMBL: M75971; AAG53459.1; -.
DR EMBL: M75967; AAG53459.1; JOINED.
DR EMBL: M75966; AAG53459.1; JOINED.
DR EMBL: M75968; AAG53459.1; JOINED.
DR EMBL: M75969; AAG53459.1; JOINED.
DR HSSP: P14210; 1BHT.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR003966; Prothrombin.
DR Pfam: PF00024; PAN. 1.
DR PRINTS: PRO0018; KRINGLE.
DR PRINTS: PRO1505; PROTHROMBIN.
DR SMART: SM00130; KR. 1.
DR SMART: SM00473; PAN_AP. 1.
DR PROSITE: PS00021; KRINGLE_1; UNKNOWN_1.
DR PROSITE: PS50070; KRINGLE_2; 1.
DR NON_TER 208 208
SQ SEQUENCE 208 AA; 23931 MW; AE9C50DE5A86B37B CRC64;

Query Match 69.3%; Score 52; DB 4; Length 208;
Best Local Similarity 72.7%; Pred. No. 0.92;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNPDGDVGGPW 11
||| : |||
Db 178 RNPGEEGGPW 188

RESULT 15

ID 013494 PRELIMINARY; PRT: 210 AA.
AC 013494;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HGF AGONIST/ANTAGONIST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96278713; PubMed-8662798;
RA Cioce V., Csaky K.G., Chan A.M.L., Bottaro D.P., Taylor W.G.,
RA Jensen R., Aaronson S.A., Rubin J.S.;
RT "Hepatocyte growth factor (HGF)/NK1 is a naturally occurring
RT HGF/scatter factor variant with partial agonist/antagonist activity.";
RL J. Biol. Chem. 271:13110-13115(1996).
DR EMBL: U46010; AAC50539.1; -.
DR HSSP: P14210; 1BHT.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR Pfam: PF00051; Kringle; 1.
DR Pfam: PF00024; PAN; 1.
DR PRINTS: PRO0018; KRINGLE.
DR PRINTS: SM00130; KR. 1.
DR SMART: SM00473; PAN_AP. 1.
DR PROSITE: PS00021; KRINGLE_1; 1.

DR PROSITE: PS50070; KRINGLE_2; 1.
SQ SEQUENCE 210 AA; 24116 MW; 9AA6BE9C50DE5A86 CRC64;

Query Match 69.3%; Score 52; DB 4; Length 210;
Best Local Similarity 72.7%; Pred. No. 0.93;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNPDGDVGGPW 11
||| : |||
Db 178 RNPGEEGGPW 188

Search completed: November 8, 2002, 09:36:10
Job time : 29.6667 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:36 ; Search time 18 Seconds
(without alignments)
64.060 Million cell updates/sec

Title: US-09-657-431-5

Perfect score: 75

Sequence: 1 RNPBGDYGVPWK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	93.3	810	1	PLHU
2	70	93.3	810	2	B30848
3	64	85.3	455	2	A61545
4	64	85.3	460	2	B61545
5	64	85.3	711	1	A47136
6	64	85.3	812	1	PIMS
7	64	85.3	812	1	PLBO
8	63	84.0	4548	1	S00657
9	60	80.0	810	2	I46260
10	57	76.0	790	1	PLPG
11	56	74.7	716	1	A40332
12	56	74.7	716	1	JC5061
13	55	73.3	625	1	TBRO
14	53	70.7	710	1	IS1283
15	52	69.3	411	2	IS1285
16	52	69.3	728	1	JH0579
17	52	69.3	728	1	A35644
18	52	69.3	728	1	A60185
19	50	66.7	169	2	A40522
20	48	64.0	336	2	S33879
21	48	64.0	508	2	F70662
22	48	64.0	617	2	S10511
23	47.5	63.3	961	2	T49228
24	47	62.7	622	1	TBHU
25	46	61.3	360	2	H70134
26	46	61.3	312	2	T46255
27	46	61.3	618	2	A38627
28	46	61.3	943	2	B45082
29	44	58.7	194	2	T10851

ALIGNMENTS

30	43.5	58.0	1420	2	A32869	apolipoprotein(a)
31	43.5	58.0	2869	2	T18518	apolipoprotein(a)
32	43.5	57.3	183	2	S05569	signaling protein
33	43.5	57.3	183	2	B90643	signaling protein
34	43.5	57.3	183	2	B85494	signaling protein
35	43.5	57.3	187	2	S26139	signaling protein
36	43.5	57.3	187	2	A48901	signaling protein
37	43.5	57.3	187	2	A10520	signaling protein
38	43.5	57.3	310	2	I50696	collagen alpha 1(I)
39	43.5	57.3	377	2	H70604	probable acyl-coA
40	43.5	57.3	534	2	F82615	methylenetetrahydrofolate
41	43.5	56.0	152	2	E87272	hypothetical prote
42	42	56.0	206	2	JC7320	K562 cell-derived
43	41.5	55.3	559	1	A35029	t-plasminogen acti
44	41.5	55.3	559	1	A29941	t-plasminogen acti
45	41.5	55.3	562	1	UKHUT	t-plasminogen acti

RESULT 1

PLHU

plasmin (EC 3.4.21.7) precursor [validated] - human

N:Alternate names: plasminogen precursor [unimonomer]

N:Contains: angiotensin; microplasmin; plasminogen

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000

C:Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625;

J. Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.

J. Biol. Chem. 265, 6104-6111, 1990

A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the f

A:Reference number: A35229; MUID:90202879

A:Accession: A35229

A:Molecule type: DNA

A:Residues: 1-810 <PEP>

A:Cross-references: GB:J05286; GB:M34276; NID:9190064; PIDN:AAA60113.1; PID:9387026

A:Experimental source: leukocyte; lung fibroblast

R:Margaret, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.;

Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990

A:Title: Definition of the transcription initiation site of human plasminogen gene in

A:Reference number: I52242; MUID:91097523

A:Accession: I52242

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-16 <MALI>

A:Cross-references: GB:M62890; NID:9190092; PIDN:AAA6454.1; PID:9553613

R:Forstren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.

FEBS Lett. 213, 254-260, 1987

A:Title: Molecular cloning and characterization of a full-length cDNA clone for human

A:Reference number: A26646; MUID:87162490

A:Accession: A26646

A:Molecule type: mRNA

A:Residues: 1-471, 'D', 'A', '73-810 <FOR>

A:Cross-references: GB:X05199; NID:935530; PIDN:CAA28831.1; PID:935531

A:Experimental source: liver

R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.

Biochemistry 23, 4243-4250, 1984

A:Title: Characterization of a full-length cDNA clone for human a

A:Reference number: I45961; MUID:85023311

A:Accession: I45961

A:Molecule type: mRNA

A:Residues: 1-62738

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 292-471, 'D', 'A', '73-810 <MAL2>

A:Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:9387031

A:Accession: I84609

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 367-419 <MAL3>

A:Cross-references: GB:K02921; NID:9190110; PIDN:AAA60123.1; PID:9190111

R:Brundish, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg,

Eur. J. Biochem. 114, 465-470, 1981

A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of huma

A:Reference number: S03735; MUID:81212097
A:Accession: S03735
A:Molecule type: Protein
A:Residues: 20-71, 'E', '73-76' <BRU>
R:Soltrup-Jensen, L.; Petersen, T.E.; Magnusson, S.
submitted to the Atlas, July 1977
A:Reference number: A00929
A:Accession: A00929
A:Molecule type: protein
A:Residues: 20-71, 'E', '73-85, 87-106', 'D', '108-360', 'E', '362-810' <SOT>
R:Wiman, B.
Eur. J. Biochem. 76, 129-137, 1977
A:Title: Primary structure of the B-chain of human plasmin.
A:Reference number: A04627; MUID:7725245
A:Accession: A04627
A:Molecule type: protein
A:Residues: 581-810 <WII>
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen activator
A:Reference number: A04625; MUID:75093329
A:Accession: A04625
A:Molecule type: protein
A:Residues: 20-50, 'Q', '51-71', 'E', '73-85, 87-100' <W12>
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen the
A:Reference number: A04626; MUID:76043692
A:Accession: A04626
A:Molecule type: protein
A:Residues: 483-507, 'E', '509-604' <W13>
R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summari, L.
J. Biol. Chem. 248, 1631-1633, 1973
A:Title: The primary structure of human plasminogen. II. The histidine loop of human plasminogen
A:Reference number: A92125; MUID:73149248
A:Contents: annotation: active site
R:Groskopf, W.R.; Summari, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
A:Reference number: A92048; MUID:69234739
A:Contents: annotation: active site
R:Trexler, M.; Vail, Z.; Pathy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
A:Reference number: A92382; MUID:82213905
A:Contents: annotation: omega-aminocarboxylic acid binding sites
R:Vail, Z.; Pathy, L.
J. Biol. Chem. 259, 13690-13694, 1984
A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
A:Reference number: A92458; MUID:85054794
A:Contents: annotation: fibrin binding site; omega-aminocarboxylic acid binding site
R:Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.;
J. Biol. Chem. 271, 29461-29467, 1996
A:Title: Kringe domains of human angiotensin. Characterization of the anti-proliferative
A:Reference number: A58811; MUID:97067211
A:Contents: annotation
R:Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A:Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (M)
A:Reference number: A58812; MUID:9548733
A:Contents: annotation
R:Tullinsky, A.; Mulichak, A.M.
submitted to the Brookhaven Protein Data Bank, July 1991
A:Reference number: A51341; PDB:1PK4
A:Contents: annotation: X-ray crystallography, 1.9 angstroms, residues 376-454
R:Tullinsky, A.; Wu, T.P.
submitted to the Brookhaven Protein Data Bank, July 1991
A:Reference number: A51488; PDB:2PK4
A:Contents: annotation: X-ray crystallography, 2.25 angstroms, residues 375-454
R:Wu, T.P.; Tullinsky, A.
submitted to the Brookhaven Protein Data Bank, August 1993
A:Reference number: A51911; PDB:1PKR

A:Contents: annotation: X-ray crystallography, 2.48 angstroms, residues 102-181
R:Padmanabhan, K.; Tullinsky, A.
submitted to the Brookhaven Protein Data Bank, April 1994
A:Reference number: A52408; PDB:1PKK
A:Contents: annotation: X-ray crystallography, 2.25 angstroms, residues 377-454
R:Tullinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A65244; PDB:1CEA
A:Contents: annotation: X-ray crystallography, 2.1 angstroms, residues 102-181
R:Tullinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A65245; PDB:1CEB
A:Contents: annotation: X-ray crystallography, 2.1 angstroms, residues 102-181
R:Mulichak, A.M.; Tullinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A:Title: Crystal and molecular structure of human plasminogen kringe 4 refined at 1.5
A:Reference number: A58819; MUID:92031502
A:Contents: annotation
R:Wu, T.P.; Padmanabhan, K.; Tullinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A:Title: The refined structure of the epsilon-aminocarboxylic acid complex of human plasminogen
A:Reference number: A58818; MUID:92031503
A:Contents: annotation
R:de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tullinsky, A.; Westbrook, R.
Biochemistry 31, 270-279, 1992
A:Title: Crystal structure of the kringe 2 domain of tissue plasminogen activator at 1.8
A:Reference number: A39483; MUID:92118803
A:Contents: annotation: X-ray crystallography, 2.4 angstroms
R:Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
submitted to the Brookhaven Protein Data Bank, June 1995
A:Reference number: A65980; PDB:1KRN
A:Contents: annotation: X-ray crystallography, 1.67 angstroms, residues 376-454
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65803; PDB:1HPJ
A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A:Title: (1)H-NMR assignments and secondary structure of human plasminogen kringe 1.
A:Reference number: A43645; MUID:94237157
A:Contents: annotation: conformation by (1)H-NMR, residues 96-184
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
A:Reference number: A58817; MUID:94237158
A:Contents: annotation: conformation by (1)H-NMR
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
A:Reference number: A58817; MUID:94237158
A:Contents: annotation: conformation by (1)H-NMR
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
A:Reference number: A58817; MUID:94237158
A:Contents: annotation: conformation by (1)H-NMR
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
A:Reference number: A58817; MUID:94237158
A:Contents: annotation: conformation by (1)H-NMR
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
A:Reference number: A58817; MUID:94237158
A:Contents: annotation: conformation by (1)H-NMR
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
A:Reference number: A58817; MUID:94237158
A:Contents: annotation: conformation by (1)H-NMR
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
A:Reference number: A58817; MUID:94237158
A:Contents: annotation: conformation by (1)H-NMR
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation: conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
A:Reference number: A58817; MUID:94237158
A:Contents: annotation: conformation by (1)H-NMR
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:

F:79-466/Product: angiotatin #status experimental <ASR>
F:97-580,581-810/Product: plasmin chain A #status experimental <MAT>
F:97-580,581-810/Product: plasmin chain A #status experimental <CHN>
F:103-181/Domains: kringle homology <KR1>
F:185-262/Domains: kringle homology <KR2>
F:275-352/Domains: kringle homology <KR3>
F:377-454/Domains: kringle homology <KR4>
F:481-560/Domains: kringle homology <KR5>
F:550-580,581-810/Product: microplasmin #status experimental <MMT>

Query Match 93.3%; Score 70; DB 1; Length 810;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNPDDGVGCPW 11
DB 532 RNPDDGVGCPW 542

RESULT 2

plasmin (EC 3.4.21.7) precursor - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C:Accession: B32869; B30848
R:Tomlinson, J.E.; McLean, J.W.; Lawm, R.M.
J Biol Chem 264, 5957-5965, 1989
A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A:Reference number: A32869; MUID:89174660
A:Accession: B32869
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-810 <TOM>

A:Cross-references: GB:J04697; NID:g342272; PIDD:AAA36901.1; PID:g342273
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-96/Domains: plasminogen-related protein precursor homology <PLPH>
F:1-9/Domains: signal sequence #status predicted <SIG>
F:103-181/Domains: kringle homology <KR1>
F:185-262/Domains: kringle homology <KR2>
F:275-352/Domains: kringle homology <KR3>
F:377-454/Domains: kringle homology <KR4>
F:481-560/Domains: kringle homology <KR5>
F:581-803/Domains: trypsin homology <TRY>
F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
bonds: #status predicted
F:622,665,760/Active site: His, Asp, Ser #status predicted

Query Match 93.3%; Score 70; DB 2; Length 810;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNPDDGVGCPW 11
DB 532 RNPDDGVGCPW 542

RESULT 3

plasmin (EC 3.4.21.7) precursor - horse (fragments)
N:Alternate names: plasminogen
N:Contains: miniplasminogen
C:Species: Equus caballus (domestic horse)
C:Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C:Accession: A61345; S17527
R:Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A:Title: Structural aspects of the plasminogen of various species.
A:Reference number: A61345; MUID:89005015
A:Accession: A61345
A:Molecule type: protein
A:Residues: 1-33;34-117 <SCH>
R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.

Protein Seq. Data Anal. 4, 69-74, 1991
A:Title: Complete amino acid sequence of equine miniplasminogen.
A:Reference number: S17527; MUID:92052077

A:Accession: S17527
A:Molecule type: protein
A:Residues: 118-455 <SC2>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
F:1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <PRO>
F:1-33/Domains: activation peptide (fragment) #status experimental <AP>
F:34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <MAT>
F:37-114/Domains: kringle homology <KR4>
F:118-455/Product: miniplasminogen #status experimental <MIN>
F:126-205/Domains: kringle homology <KR5>
F:226-455/Domains: plasmin chain B #status experimental <BCH>
F:226-448/Domains: trypsin homology <TRY>
F:267,310,405/Active site: His, Asp, Ser #status predicted

Query Match 85.3%; Score 64; DB 2; Length 455;
Best Local Similarity 90.9%; Pred. No. 0.0095;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDDGVGCPW 11
DB 177 RNPDDGVGCPW 187

RESULT 4

plasmin (EC 3.4.21.7) precursor - sheep (fragments)
N:Alternate names: plasminogen
N:Contains: miniplasminogen
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999
C:Accession: B61545; S28200
R:Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A:Title: Structural aspects of the plasminogen of various species.
A:Reference number: A61545; MUID:89005015
A:Accession: B61545
A:Molecule type: protein
A:Residues: 1-37;38-117 <SCH>
R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 5, 21-25, 1992
A:Title: Complete amino acid sequence of ovine miniplasminogen.
A:Reference number: S28200; MUID:93149955
A:Accession: S28200
A:Molecule type: protein
A:Residues: 118-460 <SC2>

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
F:1-37,38-117,118-460/Product: plasminogen (fragments) #status experimental <PRO>
F:1-37/Domains: activation peptide (fragment) #status experimental <AP>
F:38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT>
F:41-118/Domains: kringle homology <KR4>
F:118-460/Product: miniplasminogen #status experimental <MIN>
F:132-211/Domains: kringle homology <KR5>
F:226-460/Domains: plasmin chain B #status experimental <BCH>
F:231-453/Domains: trypsin homology <TRY>
F:272,315,410/Active site: His, Asp, Ser #status predicted

Query Match 85.3%; Score 64; DB 2; Length 460;
Best Local Similarity 90.9%; Pred. No. 0.0095;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDDGVGCPW 11
DB 183 RNPDDGVGCPW 193

RESULT 5

macrophage-stimulating protein 1 precursor - human
A47136

C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 #sequence-revision 14-Nov-1997 #text-change 18-Jun-1999
 C:Accession: A40331; BA0331; A47136; A61395
 R:Han, S.; Stuart, L.A.; Degen, S.J.F.
 Biochemistry 30, 9768-9780, 1991
 A:Title: Characterization of the DNF1552 locus on human chromosome 3: Identification of
 A:Reference number: A40331; MUID:92002016
 A:Accession: A40331
 A:Molecule type: DNA
 A:Residues: 1-711 <HA1>
 A:Cross-references: GB:M74179
 A:Accession: B40331
 A:Molecule type: mRNA
 A:Residues: 1-711 <HA2>
 A:Cross-references: GB:M74178; NID:Q183976; PIDN:AAA50165.1; PID:Q183977
 R:Yoshimura, T.; Yuhki, N.; Wang, M.H.; Skeel, A.; Leonard, E.J.
 J. Biol. Chem. 268, 15461-15468, 1993
 A:Title: Cloning, sequencing, and expression of human macrophage stimulating protein (MS
 A:Reference number: A47136; MUID:93340141
 A:Accession: A47136
 A:Molecule type: mRNA
 A:Residues: 1-12, 'C', 14-622, 'E', 624-711 <YOS>
 A:Cross-references: GB:LI1924; NID:Q398037; PIDN:AAA59872.1; PID:Q398038
 A:Note: authors translated the codon TTT for residue 623 as Leu; parts of this sequence
 R:Skeel, A.; Yoshimura, T.; Showalter, S.D.; Tanaka, S.; Appella, E.; Leonard, E.J.
 J. Exp. Med. 173, 1227-1234, 1991
 A:Title: Macrophage stimulating protein: purification, partial amino acid sequence, and
 A:Reference number: A61395; MUID:91217635
 A:Accession: A61395
 A:Molecule type: protein
 A:Residues: 230-247; 288-291, 'E', 293-295, 'X', 297-301, 'X', 303, 'E', 305, 'EX', 308-310; 326-331
 A:Experimental source: Plasma
 C:Genetics:
 A:Gene: GDB:MST1; D3F15S2; DNF15S2; HGFL
 A:Cross-references: GDB:188833; OMIM:142408
 A:Map position: 3p21-3p21.3
 C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
 C:Keywords: duplication; glycoprotein; growth factor; kringle; plasma
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-483/Domain: product; macrophage-stimulating protein 1 #status predicted <MAT>
 F:19-483/Domain: alpha chain #status predicted <ACH>
 F:110-186/Domain: kringle homology <KR1>
 F:191-268/Domain: kringle homology <KR2>
 F:283-361/Domain: kringle homology <KR3>
 F:370-448/Domain: kringle homology <KR4>
 F:484-711/Domain: beta chain #status predicted <BCH>
 F:484-704/Domain: trypsin homology <TRY>
 F:56-78, 60-66, 110-186, 131-169, 157-181, 191-268, 212-251, 240-263, 283-361, 304-343, 332-355, 37
 F:72, 296, 615/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 85.3%; Score 64; DB 1; Length 711;
 Best Local Similarity 90.9%; Pred. No. 0.015;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNPDGVDGCPW 11
 ||||| ||||
 DB 158 RNPDGVDGCPW 168

RESULT 6
 PLMS
 plasmin (EC 3.4.21.7) precursor - mouse
 N:Contains: angiotensin; plasminogen
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Sep-1991 #sequence-revision 01-Nov-1996 #text-change 18-Jun-1999
 C:Accession: A38514; S48202; S48203
 R:Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
 Genomics 8, 49-61, 1990
 A:Title: Characterization of the cDNA coding for mouse plasminogen and localization of t
 A:Reference number: A38514; MUID:91184812
 A:Accession: A38514
 A:Molecule type: mRNA

A:Residues: 1-812 <BRS>
 A:Cross-references: GB:J04766; NID:Q200402; PIDN:AAA50168.1; PID:Q200403
 R:Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
 Eur. J. Biochem. 224, 863-871, 1994
 A:Title: Characterization of the murine plasma fibrinolytic system.
 A:Reference number: S48202; MUID:95010076
 A:Accession: S48202
 A:Molecule type: protein
 A:Residues: 20-25 <LIJ>
 A:Accession: S48203
 A:Molecule type: protein
 A:Residues: 22-27 <LI2>
 C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many
 C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plas
 C:Comment: immediately after dissociation from the clot. In the presence of the inhibitor, the act
 C:Comment: inhibitor. The activation involves also removal of the activation peptide.
 C:Comment: Streptolysin I (see PIR:KCMS1) acts on plasminogen to produce angiotensin.
 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
 C:Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; h
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-812/Product: plasminogen #status predicted <PRO>
 F:20-96/Domain: activation peptide #status predicted <APT>
 F:79-466/Product: angiotensin #status predicted <AST>
 F:97-581, 582-812/Product: plasmin #status predicted <MAT>
 F:97-581/Domain: chain A #status predicted <ACH>
 F:103-181/Domain: kringle homology <KR1>
 F:185-262/Domain: kringle homology <KR2>
 F:275-352/Domain: kringle homology <KR3>
 F:377-454/Domain: kringle homology <KR4>
 F:481-560/Domain: kringle homology <KR5>
 F:582-812/Domain: chain B #status predicted <BCH>
 F:582-805/Domain: trypsin homology <TRY>
 F:49-73, 53-61, 103-181, 124-164, 152-176, 185-262, 188-316, 206-245, 234-257, 275-352, 296-335
 F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
 F:136, 308/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted
 F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
 F:624, 667, 762/Active site: His, Asp, Ser #status predicted
 Query Match 85.3%; Score 64; DB 1; Length 812;
 Best Local Similarity 90.9%; Pred. No. 0.018;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNPDGVDGCPW 11
 ||||| ||||
 DB 532 RNPDGVDGCPW 542

RESULT 7
 PLBO
 plasmin (EC 3.4.21.7) precursor - bovine
 N:Alternate names: plasminogen
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1987 #sequence-revision 28-Apr-1995 #text-change 18-Jun-1999
 C:Accession: S45046; A25835; I45961; S03736
 R:Berglund, L.; Andersen, M.D.; Petersen, T.E.
 submitted to the EMBL data library, May 1994
 A:Description: Cloning and characterization of the bovine plasminogen cDNA.
 A:Reference number: S45046
 A:Accession: S45046
 A:Molecule type: mRNA
 A:Residues: 1-812 <BRS>
 A:Cross-references: EMBL:X79402; NID:Q494962; PIDN:CAA55939.1; PID:Q494963
 A:Experimental source: liver
 A:Note: it is uncertain whether Met-1 or Met-8 is the initiator
 R:Schaller, J.; Moser, P.W.; Danneberg-Muller, G.A.K.; Rossetti, S.J.; Kampfer, U.; R

Eur. J. Biochem. 149, 267-278, 1985
A>Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasminogen.
A:Reference number: A25835; MUID:85203906
A:Accession: A25835
A:Molecule type: protein
A:Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A>Title: Characterization of a complementary deoxyribonucleic acid coding for human and mouse plasminogen.
A:Reference number: 145961; MUID:85023311
A:Accession: 145961
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 706-743, 'R', 745-812 <MAL>
A:Cross-references: GB:K02935; NID:g163551; PIDN:AAA30714.1; PID:g163552
R:Brinistolz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.; Eur. J. Biochem. 114, 465-470, 1981
A>Title: Comparison of the primary structure of the N-terminal CNBR fragments of human, mouse, and rat plasminogen.
A:Reference number: S03735; MUID:81212097
A:Accession: S03735
A:Molecule type: protein
A:Residues: 27-83

C:Function:
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of the granular follicle; also activates the urokinase-type plasminogen activator.
A:Pathway: fibrinolysis
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; F/1-26/Domain: signal sequence #status predicted <SIG>
F/8-103/Domain: plasminogen-related protein precursor homology <PLP>
F/27-812/Domain: plasminogen #status experimental <PRO>
F/27-103/Domain: activation peptide #status experimental <APT>
F/104-583,584-812/Product: plasmin #status experimental <MAT>
F/110-583/Domain: plasmin chain A #status experimental <ACH>
F/110-188/Domain: plasmin chain B #status experimental <ACH>
F/192-269/Domain: kringle homology <KR2>
F/282-359/Domain: kringle homology <KR3>
F/384-461/Domain: kringle homology <KR4>
F/485-564/Domain: kringle homology <KR5>
F/584-812/Domain: plasmin chain B #status experimental <BCH>
F/584-805/Domain: trypsin homology <TRY>
F/56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,333-342/Domain: #status predicted
F/315/Binding site: carbohydrate (asn) (covalent) #status experimental
F/365/Binding site: carbohydrate (ser) (covalent) #status experimental
F/624,667,762/Active site: His, Asp, Ser #status predicted
Query Match 85.3%; Score 64; DB 1; Length 812;
Best Local Similarity 90.9%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RNPDDVGGPW 11
DB 536 RNPDDVGGPW 546
RESULT 8
S00657
apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
N:Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 08-Dec-2000
C:Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286
R:McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, G.M.; Scarl Nature 330, 132-137, 1987
A>Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
A:Reference number: S00657; MUID:88039109
A:Accession: S00657
A:Molecule type: mRNA
A:Residues: 1-4548 <MCL>
A:Cross-references: GB:X06290; EMBL:X06696; NID:g28619; PIDN:CAA29618.1; PID:g28620
R:Paton, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Law, R.M. Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987

A>Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to plasminogen.
A:Reference number: A28017; MUID:87204109
A:Accession: A28017
A:Molecule type: protein
A:Residues: 20-21, 'P', 23-34, 177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200-292-314, 'W', 316 'X', 4396-4401 <EAT>
R:Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Schwartz Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A>Title: 5' control regions of the apolipoprotein(a) gene and members of the related gene family.
A:Reference number: A47277; MUID:93165698
A:Accession: A47277
A>Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:I07899; NID:g967973; PID:g967974
R:Margaret, N.; Acquati, F.; Magnani, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sa Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A>Title: Characterization by yeast artificial chromosome cloning of the linked apolipoprotein(a) gene and members of the related gene family.
A:Reference number: A47233; MUID:93087573
A:Accession: 160906
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:M90078; NID:g178786; PIDN:AAA35547.1; PID:g553188
A:Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: A47233
A>Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:M90079; NID:g178784; PIDN:AAA35546.1; PID:g553187
R:Ichinohe, A.
Biochemistry 31, 3113-3118, 1992
A>Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated with the human chromosome 6p21.
A:Reference number: I52415; MUID:92207924
A:Accession: I52415
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:M86877; NID:g178780; PIDN:AAA49909.1; PID:g553185
A:Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: 165286
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:M86878; NID:g178782; PIDN:AAA51749.1; PID:g553186
C:Genetics:
A:Gene: GDB:LPA
A:Cross-references: GDB:120699; OMIM:152200
A:Map position: 6q26-q27
A:Note: several genes closely linked on chromosome 6 are identical in the first codons of kringle repeats
C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C:Keywords: hydrolase; kringle; signal sequence #status predicted <SIG>
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-4548/Product: apolipoprotein(a) #status experimental <MAT>
F/28-105/Domain: kringle homology <KR1>
F/142-219/Domain: kringle homology <KR2>
F/256-333/Domain: kringle homology <KR3>
F/370-447/Domain: kringle homology <KR4>
F/484-561/Domain: kringle homology <KR5>
F/598-675/Domain: kringle homology <KR6>
F/712-789/Domain: kringle homology <KR7>
F/826-903/Domain: kringle homology <KR8>
F/940-1017/Domain: kringle homology <KR9>
F/1054-1131/Domain: kringle homology <KR10>
F/1168-1245/Domain: kringle homology <KR11>
F/1282-1359/Domain: kringle homology <KR12>
F/1396-1473/Domain: kringle homology <KR13>
F/1510-1587/Domain: kringle homology <KR14>
F/1624-1701/Domain: kringle homology <KR15>
F/1738-1815/Domain: kringle homology <KR16>
F/1852-1929/Domain: kringle homology <KR17>
F/1966-2043/Domain: kringle homology <KR18>

F:2080-2157/Domain: kringle homology <KR19>
 F:2194-2271/Domain: kringle homology <KR20>
 F:2308-2385/Domain: kringle homology <KR21>
 F:2422-2499/Domain: kringle homology <KR22>
 F:2536-2613/Domain: kringle homology <KR23>
 F:2650-2727/Domain: kringle homology <KR24>
 F:2764-2841/Domain: kringle homology <KR25>
 F:2878-2955/Domain: kringle homology <KR26>
 F:2992-3069/Domain: kringle homology <KR27>
 F:3106-3183/Domain: kringle homology <KR28>
 F:3220-3297/Domain: kringle homology <KR29>
 F:3334-3411/Domain: kringle homology <KR30>
 F:3448-3525/Domain: kringle homology <KR31>
 F:3562-3639/Domain: kringle homology <KR32>
 F:3676-3753/Domain: kringle homology <KR33>
 F:3782-3859/Domain: kringle homology <KR34>
 F:3896-3973/Domain: kringle homology <KR35>
 F:4010-4087/Domain: kringle homology <KR36>
 F:4124-4201/Domain: kringle homology <KR37>
 F:4228-4307/Domain: kringle homology <KR38>
 F:4328-4541/Domain: trypsin homology <TRY>

Query Match 84.0%; Score 63; DB 1; Length 4548;
 Best Local Similarity 81.8%; Pred. No. 0.16;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 RNPDGDVGCPW 11
 Db 4279 RNPDGDINGPW 4289

RESULT 9
 16260
 plasmin (EC 3.4.21.7) precursor - western European hedgehog
 C:Species: Erinaceus europaeus (western European hedgehog)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C:Accession: I6260
 R:Lauw, K.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong
 J. Biol. Chem. 270, 24004-24009, 1995
 A>Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein
 A:Reference number: I46259; MUID:96025778
 A:Accession: I46260
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-810 <LAW>
 A:Cross-references: EMBL:U33171; NID:91046360; PID:91046361
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: hydrolase; serine proteinase
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>
 F:103-181/Domain: kringle homology <KR1>
 F:185-262/Domain: kringle homology <KR2>
 F:275-352/Domain: kringle homology <KR3>
 F:379-456/Domain: kringle homology <KR4>
 F:482-561/Domain: kringle homology <KR5>
 F:582-803/Domain: trypsin homology <TRY>

Query Match 80.0%; Score 60; DB 2; Length 810;
 Best Local Similarity 81.8%; Pred. No. 0.079;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 RNPDGDVGCPW 11
 Db 533 RNPDGDANGPW 543

RESULT 10
 PLPG
 plasmin (EC 3.4.21.7) precursor - pig (fragment)
 N:Alternate names: plasminogen
 N:Contains: miniplasminogen
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
 C:Accession: S03733; S03737; A25834

R:Schaller, J.; Marti, T.; Roeselelet, S.J.; Kaempfer, U.; Rickli, E.E.
 Fibrinolysis 1, 91-102, 1987
 A>Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the
 A:Reference number: S03733
 A:Accession: S03733
 A:Molecule type: protein
 A:Residues: 1-560 <SCH>
 R:Brundholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg,
 Eur. J. Biochem. 114, 465-470, 1981
 A>Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma
 A:Reference number: S03735; MUID:81212097
 A:Accession: S03737
 A:Molecule type: protein
 A:Residues: 1-57 <BRU>
 R:Marti, T.; Schaller, J.; Rickli, E.E.
 Eur. J. Biochem. 149, 279-285, 1985
 A>Title: Determination of the complete amino-acid sequence of porcine miniplasminogen
 A:Reference number: A25834; MUID:85203907
 A:Accession: A25834
 A:Molecule type: protein
 A:Residues: 450-790 <MAR>
 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a
 us the walls of the graafian follicle; also activates the urokinase-type plasminogen
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine pr
 F:1-90/Product: plasminogen #status predicted <PRO>
 F:1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
 F:78-560/Product: activation peptide #status predicted <AP>
 F:84-162/Domain: kringle homology <KR1>
 F:166-243/Domain: kringle homology <KR2>
 F:256-333/Domain: kringle homology <KR3>
 F:338-435/Domain: kringle homology <KR4>
 F:450-790/Product: miniplasminogen #status experimental <MIN>
 F:461-540/Domain: kringle homology <KR5>
 F:561-790/Product: plasmin chain B #status experimental <BCH>
 F:561-783/Domain: trypsin homology <TRY>
 F:30-54, 34-42, 84-162, 105-145, 133-157, 166-243, 169-297, 187-226, 215-238, 256-333, 277-316,
 bonds: #status predicted
 F:602, 645, 740/Active site: His, Asp, Ser #status predicted

Query Match 76.0%; Score 57; DB 1; Length 790;
 Best Local Similarity 81.8%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 RNPDGDVGCPW 11
 Db 512 RNPDGDNGCPW 522

RESULT 11
 A40332
 macrophage-stimulating protein 1 precursor - mouse
 N:Alternate names: hepatocyte growth factor-like protein
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1999
 C:Accession: A40332; B40332
 R:Deegen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
 Biochemistry 30, 9781-9791, 1991
 A>Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth f
 A:Reference number: A40332; MUID:92002017
 A:Accession: A40332
 A:Molecule type: DNA
 A:Residues: 1-716 <DEG>
 A:Cross-references: GB:M4180; NID:9193831; PID:AAA50166.1; PID:9193832
 A:Accession: B40332
 A:Molecule type: mRNA
 A:Residues: 1-18, 'P', '20'-716 <DEG>
 A:Cross-references: GB:M4181; NID:9193833; PID:AAA50167.1; PID:9193834
 C:Genetics:
 A:introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1;

C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
 C:Keywords: duplication; glycoprotein; growth factor; kringle
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:19-488/489-716/Product: macrophage-stimulating protein 1 #status experimental <MAC>
 F:19-483/Domain: alpha chain #status experimental <ACH>
 F:110-186/Domain: kringle homology <KR1>
 F:191-268/Domain: kringle homology <KR2>
 F:292-370/Domain: kringle homology <KR3>
 F:379-457/Domain: kringle homology <KR4>
 F:484-711/Domain: beta chain #status experimental <BCH>
 F:489-709/Domain: trypsin homology <TRY>
 F:72,173,305,620/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 74.7%; Score 56; DB 1; Length 716;
 Best Local Similarity 81.8%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 429 RNPDDGVGSPW 11
 1 RNPDDGVGSPW 439

RESULT 12
 JCS061
 macrophage-stimulating protein 1 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000
 C:Accession: JCS061
 R:Ohshiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takasu, N.
 Biochem. Biophys. Res. Commun. 227, 273-280, 1996
 A:Title: Molecular cloning of rat macrophage-stimulating protein and its involvement in
 A:Reference number: JCS061; MUID:97011126
 A:Accession: JCS061
 A:Molecule type: mRNA
 A:Residues: 1-716 <OHS>
 A:Cross-references: EMBL:X95096; NID:q1669718; PIDN:CA64473.1; PID:q1669719
 C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
 C:Keywords: duplication; glycoprotein; growth factor; kringle
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-488/489-716/Product: macrophage-stimulating protein 1 #status predicted <MAT>
 F:32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>
 F:110-186/Domain: kringle homology <KR1>
 F:191-268/Domain: kringle homology <KR2>
 F:292-370/Domain: kringle homology <KR3>
 F:379-457/Domain: kringle homology <KR4>
 F:489-709/Domain: trypsin homology <TRY>
 F:72,305,620/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 74.7%; Score 56; DB 1; Length 716;
 Best Local Similarity 81.8%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 429 RNPDDGVGSPW 11
 1 RNPDDGVGSPW 439

RESULT 13
 TB0
 thrombin (EC 3.4.21.5) precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Apr-1984 #sequence_revision 14-Jul-1994 #text_change 18-Jun-1999
 C:Accession: S02537; A00915; A37552; I46045; S67518
 R:Irwin, D.M.; Robertson, K.A.; Macgillivray, R.T.A.
 J. Mol. Biol. 200, 31-45, 1988
 A:Title: Structure and evolution of the bovine prothrombin gene.
 A:Reference number: S02537; MUID:86245190
 A:Accession: S02537
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA

Query Match 73.3%; Score 55; DB 1; Length 625;
 Best Local Similarity 72.7%; Pred. No. 0.4;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

A:Residues: 1-625 <IRW>
 R:Macgillivray, R.T.A.; Davie, E.W.
 Biochemistry 23, 1626-1634, 1984
 A:Title: Characterization of bovine prothrombin mRNA and its translation product.
 A:Reference number: A00915; MUID:84203525
 A:Accession: A00915
 A:Molecule type: mRNA
 A:Residues: 1-230, 'H', 232-625 <MAC>
 A:Note: 600-Asn was also found
 R:Macgillivray, R.T.A.; Petersen, T.E.; Claeys, H.
 In Boerhaave Symposium on Prothrombin and Related Coagulation Factors, Hemker, H.C.,
 A:Reference number: A37552
 A:Accession: A37552
 A:Molecule type: Protein
 A:Residues: 44-287, 'N', 289-352, 'E', 354, 'Q', 356-548, 'ND', 551-599, 'N', 601-625 <MAC>
 A:Note: The evidence for 231-Ser is strong
 A:Note: disulfide bonds and carbohydrate binding sites were determined
 R:Park, C.H.; Tulinsky, A.
 Biochemistry 25, 3977-3982, 1986
 A:Title: Three-dimensional structure of the kringle sequence: structure of prothrombin
 A:Reference number: A37553; MUID:86296631
 A:Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms
 R:Irwin, D.M.; Ahern, K.G.; Pearson, G.D.; Macgillivray, R.T.A.
 Biochemistry 24, 6854-6861, 1985
 A:Title: Characterization of the bovine prothrombin gene.
 A:Reference number: A37554; MUID:86077733
 A:Contents: annotation; gene structure
 R:Macgillivray, R.T.; Degen, S.J.; Chandra, T.; Woo, S.L.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980
 A:Title: Cloning and analysis of a cDNA coding for bovine prothrombin.
 A:Reference number: I46045; MUID:81054926
 A:Accession: I46045
 A:Status: preliminary; translated from GR/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 466-599, 'N', 601-625 <MA2>
 A:Cross-references: EMBL:V00135; NID:9772; PIDN:CA23451.1; PID:9808945
 R:Pejler, G.; Karlstroem, A.R.; Berg, L.
 Eur. J. Biochem. 227, 102-107, 1995
 A:Title: Identification of the proteolytic thrombin fragments formed after cleavage w
 A:Reference number: S67518; MUID:95154277
 A:Accession: S67518
 A:Status: preliminary
 A:Molecule type: Protein
 A:Residues: 318-325,333-338, 'X', 340;367-374;481-484, 'X', 486-488;515-522 <PEJ>
 C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fi
 C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that bi
 C:Comment: Prothrombin is activated on the surface of a phospholipid membrane. The acti
 C:Comment: Thrombin can cleave the amino-terminal activation peptide 1 from prothrombi
 C:Comment: The gamma-carboxyglutamate residues bind calcium ions, result from the carb
 C:Comment: The prothrombin precursor is synthesized in the liver.
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; duplication; gl
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-43/Domain: propeptide #status predicted <PRO>
 F:28-88/Domain: Gla domain homology <GLA>
 F:44-625/Product: prothrombin #status experimental <MPT>
 F:44-199/Domain: activation peptide 1 #status experimental <FR1>
 F:109-187/Domain: kringle homology <KR1>
 F:200-317/Domain: activation peptide 2 #status experimental <FR2>
 F:214-292/Domain: kringle homology <KR2>
 F:318-366/Product: thrombin light chain #status experimental <LCH>
 F:367-625/Product: thrombin heavy chain #status experimental <HCH>
 F:367-616/Domain: trypsin homology <TRY>
 F:50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:61-66,91-104,109-187,130-170,158-182,214-292,235-275,263-287,339-485,394-410,539-55
 F:120,144,419/Binding site: carbohydrate (asn) (covalent) #status experimental
 F:409,465,571/Active site: His, Asp, Ser #status experimental

QY 1 RNPDGVDGCPW 11
 |||| : |||
 Db 159 RNPDGSGTGPW 169

RESULT 14

151283
 hepatocyte growth factor precursor - clawed frog
 N:Alternate names: hepatoleitin A; scatter factor
 C:Species: Xenopus sp. (clawed frog)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
 C/Accession: I51283
 R:Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiohawa, K.
 Mech. Dev. 49, 123-131, 1995
 A:Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus ear
 A:Reference number: I51283; MUID:95267690
 A:Accession: I51283
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-710 <NAK>
 A:Cross-references: GB:S77422; NID:9998932; PIDN:AAB34354.1; PID:9998933
 A:Note: the authors' translation for residue 458 (Thr) is inconsistent with the nucleot
 C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C:Function:
 A:Description: stimulates mitosis of hepatocytes and other cells
 A:Note: does not have proteinase activity
 C:Superfamily: hepatocyte growth factor; kringe homology; trypsin homology
 C:Keywords: duplication; glycoprotein; growth factor; heterodimer; kringe
 F:42-477,478-709/Product: hepatocyte growth factor #status predicted <MAT>
 F:42-477/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
 F:115-193/Domain: kringe homology <KR1>
 F:198-275/Domain: kringe homology <KR2>
 F:289-367/Domain: kringe homology <KR3>
 F:375-453/Domain: kringe homology <KR4>
 F:478-709/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
 F:478-700/Domain: trypsin homology <TRY>
 F:52,128,281,322,379,550,637,666/Binding site: carbohydrate (Asn) (covalent) #status pre
 F:470-588/Disulfide bonds: #status predicted

Query Match 70.7%; Score 53; DB 1; Length 710;
 Best Local Similarity 72.7%; Pred. No. 0.97;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RNPDGVDGCPW 11
 |||| : |||
 Db 165 RNPDGSGTGPW 175

RESULT 15

151285
 hepatocyte growth factor/scatter factor - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C/Accession: I51285
 R:Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard
 Development 121, 813-824, 1995
 A:Title: A role for HGF/SF in neural induction and its expression in Hensen's node durin
 A:Reference number: I51285; MUID:95237013
 A:Accession: I51285
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-411 <SNR>
 A:Cross-references: GB:S77480; NID:9998675; PID:9998676
 C:Superfamily: hepatocyte growth factor; kringe homology; trypsin homology
 F:124-197/Domain: kringe homology <KR6>
 F:202-279/Domain: kringe homology <KR2>
 F:296-374/Domain: kringe homology <KR3>

Query Match 69.3%; Score 52; DB 2; Length 411;
 Best Local Similarity 72.7%; Pred. No. 0.79;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNPDGVDGCPW 11
 |||| : |||
 Db 169 RNPDGSGTGPW 179

Search completed: November 8, 2002, 09:36:44
 Job time : 19 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:33:21 ; Search time 9.3333 Seconds

(Without alignments)
49.782 Million cell updates/sec

Title: US-09-657-431-5

Perfect score: 75

Sequence: 1 RMPDGDVGGPFWK 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	93.3	810	1 PLMN_HUMAN	P00747 homo sapien
2	70	93.3	810	1 PLMN_MACMU	P12545 macaca mula
3	64	85.3	333	1 PLMN_CANFA	P80009 canis fami
4	64	85.3	338	1 PLMN_HORSE	P80010 equus cabal
5	64	85.3	343	1 PLMN_SHEEP	P81286 ovis aries
6	64	85.3	711	1 HGFL_HUMAN	P26927 homo sapien
7	64	85.3	812	1 PLMN_BOVIN	P06868 bos taurus
8	64	85.3	812	1 PLMN_MOUSE	P20918 mus musculu
9	63	84.0	4548	1 APOA_HUMAN	P08519 homo sapien
10	60	80.0	810	1 PLMN_ERIEU	O29485 erinaceus e
11	57	76.0	790	1 PLMN_PIG	P06867 sus scrofa
12	56	74.7	716	1 HGFL_MOUSE	P26928 mus musculu
13	55	73.3	625	1 THRB_BOVIN	P00735 bos taurus
14	52	69.3	728	1 HGF_HUMAN	P14210 homo sapien
15	52	69.3	728	1 HGF_MOUSE	O08048 mus musculu
16	52	69.3	728	1 HGF_MOUSE	P17945 rattus norv
17	50	66.7	169	1 PLMN_RAT	O01177 rattus norv
18	48	64.0	325	1 PLMN_PERMA	P33574 petromyzon
19	48	64.0	517	1 PHLC_MYCTU	P95245 mycobacteri
20	48	64.0	617	1 THRB_RAT	P18292 rattus norv
21	47.5	63.3	961	1 PM77_ARATH	O91932 arabidopsis
22	47	62.7	622	1 THRB_HUMAN	P00734 homo sapien
23	46	61.3	618	1 THRB_MOUSE	P19221 mus musculu
24	46	61.3	943	1 ROR2_HUMAN	O01974 homo sapien
25	46	61.3	944	1 ROR2_MOUSE	O92138 mus musculu
26	44	58.7	194	1 Y4HQ_RHISN	P50363 rhizobium s
27	43.5	58.0	1420	1 APOA_MACMU	P14417 macaca mula
28	43	57.3	183	1 AMPD_ECOLI	P13016 escherichia
29	43	57.3	187	1 AMPD_CITFR	P82973 citrobacter
30	43	57.3	187	1 AMPD_ENTCL	P82973 enterobacte
31	43	57.3	187	1 AMPD_SALTY	P30013 salmonella
32	41.5	55.3	559	1 TPA_MOUSE	P11214 mus musculu
33	41.5	55.3	559	1 TPA_RAT	P19637 rattus norv

34	41.5	55.3	562	1 TPA_HUMAN	P00750 homo sapien
35	41.5	55.3	566	1 TPA_BOVIN	O28198 bos taurus
36	41	54.7	1089	1 UBP6_HUMAN	P35125 homo sapien
37	41	54.7	1748	1 POLR_ELV	P35928 erythrum la
38	41	54.7	1822	1 ZAP3_HUMAN	P49370 homo sapien
39	40	53.3	285	1 PNMT_RAT	P10937 rattus norv
40	40	53.3	295	1 PNMT_MOUSE	P40935 mus musculu
41	40	53.3	1262	1 CA13_CHICK	P12105 gallus gall
42	39	52.0	102	1 SGP3_CHRV1	O52055 chromatium
43	39	52.0	209	1 VP32_BPAPS	O91176 bacterioph
44	39	52.0	283	1 CC19_CABEL	P18835 caenorhabdi
45	39	52.0	399	1 IRTF_MOUSE	O61179 mus musculu

ALIGNMENTS

RESULT 1	PLMN_HUMAN	STANDARD;	PRT;	810 AA.
ID	PLMN_HUMAN			
AC	P00747;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-MAR-1989 (Rel. 10, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Plasminogen precursor (EC 3.4.21.7) [contains: Angiostatin].			
GN	PLG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90202879; PubMed=2318848;			
RA	Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;			
RT	Characterization of the gene for human plasminogen, a key proenzyme			
RT	in the fibrinolytic system.";			
RL	J. Biol. Chem. 265:6104-6111(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87162490; PubMed=3030813;			
RA	Forsgren M., Raden B., Israelsson M., Larsson K., Hedén L.-O.;			
RT	"Molecular cloning and characterization of a full-length cDNA clone			
RT	for human plasminogen.";			
RL	FEBS Lett. 213:254-260(1987).			
RN	[3]			
RP	SEQUENCE OF 20-810.			
RA	Sottrop-Jensen L., Petersen T.E., Magnusson S.;			
RT	Submitted (JUL-1977) to the PIR data bank.			
RL	[4]			
RP	SEQUENCE OF 292-810 FROM N.A.			
RX	MEDLINE=85023311; PubMed=6148961;			
RA	Mallinowski D.P., Sadler J.E., Davie E.W.;			
RT	"Characterization of a complementary deoxyribonucleic acid coding for			
RT	human and bovine plasminogen.";			
RL	Biochemistry 23:4243-4250(1984).			
RN	[5]			
RP	SEQUENCE OF 20-100.			
RX	MEDLINE=75093329; PubMed=122932;			
RA	Wiman B., Wallen P.;			
RT	"Structural relationship between 'glutamic acid' and 'lysine' forms			
RT	of human plasminogen and their interaction with the NH2-terminal			
RT	activation peptide as studied by affinity chromatography.";			
RL	Eur. J. Biochem. 50:489-494(1975).			
RN	[6]			
RP	SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810.			
RA	Sottrop-Jensen L., Claess H., Zajdel M., Petersen T.E., Magnusson S.;			
RT	(in) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);			
RT	Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,			
RL	Raven Press, New York (1978).			
RN	[7]			
RP	SEQUENCE OF 483-604.			
RA	MEDLINE=76043692; PubMed=126863;			
RL	Wiman B., Wallen P.;			

- RT "Amino-acid sequence of the cyanogen-bromide fragment from human
RT plasminogen that forms the linkage between the plasmin chains.";
RL Eur. J. Biochem. 58:539-547(1975).
RN [8]
RP SEQUENCE OF 581-810.
RX MEDLINE-77225245; PubMed-142009;
RA Wiman B.;
RT "Primary structure of the B-chain of human plasmin.";
RL Eur. J. Biochem. 76:129-137(1977).
RN [9]
RP ACTIVE SITE.
RX MEDLINE-73149248; PubMed-4694729;
RX Robbins K.C., Bernabe P., Arzadon L., Summaria L.;
RT "The primary structure of human plasminogen. II. The histidine loop
RT of human plasmin: light (B) chain active center histidine sequence.";
RL J. Biol. Chem. 248:1631-1633(1973).
RN [10]
RP ACTIVE SITE.
RX MEDLINE-69234739; PubMed-4240117;
RX Groskopf W.R., Summaria L., Robbins K.C.;
RT "Studies on the active center of human plasmin. Partial amino acid
RT sequence of a peptide containing the active center serine residue.";
RL J. Biol. Chem. 244:3590-3597(1969).
RN [11]
RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RX MEDLINE-82213905; PubMed-6919539;
RX Trexler M., Vali Z., Patchy L.;
RT "Structure of the omega-aminocarboxylic acid-binding sites of human
RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
RT binding of ligand by kringle 4.";
RL J. Biol. Chem. 257:7401-7406(1982).
RN [12]
RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RX MEDLINE-85054794; PubMed-6094526;
RA Vali Z., Patchy L.;
RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
RT are essential for fibrin affinity of the kringle 1 domain.";
RL J. Biol. Chem. 259:13690-13694(1984).
RN [13]
RP PHOSPHORYLATION SITE SER-597.
RX MEDLINE-97345939; PubMed-9201958;
RX Wang H., Protor M., Brethauer R.K., Castellino F.J.;
RT "Serine-578 is a major phosphorylation locus in human plasma
RT plasminogen.";
RL Biochemistry 36:8100-8106(1997).
RN [14]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE-88185329; PubMed-3356193;
RX Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63(1988).
RN [15]
RP CARBOHYDRATE-LINKAGE SITE 268.
RX MEDLINE-97207306; PubMed-9054441;
RX Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,
RA Pizzo S.V.;
RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
RT human plasminogen 2.";
RL J. Biol. Chem. 272:7408-7411(1997).
RN [16]
RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RX MEDLINE-95042728; PubMed-755077;
RX O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RA Mosses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma.";
RL Cell 79:315-328(1994).
RN [17]
RP CHARACTERIZATION OF ANGIOSTATIN.
RX MEDLINE-97238710; PubMed-9102221;
RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
RA Lapcevic R., Nacy C.A.;
RT "A recombinant human angiotensin protein inhibits experimental primary
RT and metastatic cancer.";
RL Cancer Res. 57:1329-1334(1997).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RX MEDLINE-92031502; PubMed-1657148;
RX Mulichak A.M., Tulinsky A., Ravichandran K.G.;
RT "Crystal and molecular structure of human plasminogen kringle 4
RT refined at 1.9-A resolution.";
RL Biochemistry 30:10576-10588(1991).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RX MEDLINE-92031503; PubMed-1657149;
RX Wu T.P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of
RT human plasminogen kringle 4.";
RL Biochemistry 30:10589-10594(1991).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RX Stec B., Yamano A., Whitlow M., Teeter M.M.;
RT Submitted (JUN-1995) to the PDB data bank.
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
RX MEDLINE-96180681; PubMed-8611560;
RX Mathews I.I., Vanderhoff-Hanover P., Castellino F.J., Tulinsky A.;
RT "Crystal structures of the recombinant kringle 1 domain of human
RT plasminogen in complexes with the ligands epsilon-aminocaproic acid
RT and trans-4-(aminomethyl)cyclohexane-1-carboxylic acid.";
RL Biochemistry 35:2567-2576(1996).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
RX MEDLINE-98198034; PubMed-9521645;
RX Chang Y., Mochalkin I., Mccance S.G., Cheng B., Tulinsky A.,
RA Castellino F.J.;
RT "Structure and ligand binding determinants of the recombinant kringle
RT 5 domain of human plasminogen.";
RL Biochemistry 37:3258-3271(1998).
RN [23]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE-94237157; PubMed-8181475;
RX Rejzante M.R., Llinas M.;
RT "1H-NMR assignments and secondary structure of human plasminogen
RT kringle 1.";
RL Eur. J. Biochem. 221:927-937(1994).
RN [24]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE-94237158; PubMed-8181476;
RX Rejzante M.R., Llinas M.;
RT "Solution structure of the epsilon-aminohexanoic acid complex of
RT human plasminogen kringle 1.";
RL Eur. J. Biochem. 221:939-949(1994).
RN [25]
RP STRUCTURE BY NMR OF 183-354.
RX MEDLINE-96194156; PubMed-8652577;
RX Soehnel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
RA Rickli E.E.;
RT "Recombinant gene expression and 1H NMR characteristics of the
RT kringle (2 + 3) supermodule: spectroscopic/functional individuality
RT of plasminogen kringle domains.";
RL Biochemistry 35:2357-2364(1996).
RN [26]
RP STRUCTURE BY NMR OF 374-461.
RX MEDLINE-90219023; PubMed-2157850;
RX Atkinson R.A., Williams R.J.P.;
RT "Solution structure of the kringle 4 domain from human plasminogen by
RT 1H nuclear magnetic resonance spectroscopy and distance geometry.";
RL J. Mol. Biol. 212:541-552(1990).
RN [27]
RP VARIANTS PHE-374 AND THR-620.
RX MEDLINE-91095410; PubMed-1986355;
RX Ichinose A., Espling E.S., Takamatsu J., Saito H., Shimoyozu K.,

Query Match 93.3%; Score 70; DB 1; Length 810;
 Best Local Similarity 100.0%; Pred. No. 0.00078;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNPDDGVGGPW 11
 |||||
 Db 532 RNPDDGVGGPW 542

RESULT 2
 PLNN_MACMU STANDARD; PRT; 810 AA.
 AC P12545;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7).
 GN PLG.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89174660; PubMed=2925643;
 RA Tomlinson J.E., McLean J.W., Lawn R.M.;
 RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
 synthesis";
 RL J. Biol. Chem. 264:5957-5965(1989).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION. IT WEAKENS THE WALLS OF THE
 GRAFVIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
 INVOLVES ONLY CLEAVAGE AFTER ARG-580, RESULTING IN 2 CHAINS HELD
 TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
 ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
 CC -----
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 or send an email to license@sdb.ch).
 CC -----
 CC EMBL: J04697; AAA36901.1; -
 DR PIR: B30848; B30848.
 DR PIR: B32869; B32869.
 DR HSSP: P00747; 1PMK.
 DR MEROPS: S01.233; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; Kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.

DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR: 4.
 DR SMART: SM00473; PAN_AP: 1.
 DR SMART: SM00020; TRYP_SPE: 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS50070; KRINGLE_2; 5.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 810 PLASMINOGEN.
 FT CHAIN 20 580 PLASMIN HEAVY CHAIN A.
 FT PEPTIDE 20 96 ACTIVATION PEPTIDE.
 FT CHAIN 97 580 PLASMIN SHORT FORM OF CHAIN A.
 FT CHAIN 581 810 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 103 181 KRINGLE 1.
 FT DOMAIN 184 262 KRINGLE 2.
 FT DOMAIN 275 352 KRINGLE 3.
 FT DOMAIN 377 454 KRINGLE 4.
 FT DOMAIN 481 560 KRINGLE 5.
 FT DOMAIN 581 810 SERINE PROTEASE.
 FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
 FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
 FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
 FT BINDING 136 136 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 138 138 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 172 172 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 432 432 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 445 445 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 134 134 FIBRIN.
 FT BINDING 136 136 FIBRIN.
 FT DISULFID 49 73 BY SIMILARITY.
 FT DISULFID 53 61 BY SIMILARITY.
 FT DISULFID 103 181 BY SIMILARITY.
 FT DISULFID 124 164 BY SIMILARITY.
 FT DISULFID 152 176 BY SIMILARITY.
 FT DISULFID 185 262 BY SIMILARITY.
 FT DISULFID 188 316 BY SIMILARITY.
 FT DISULFID 206 245 BY SIMILARITY.
 FT DISULFID 234 257 BY SIMILARITY.
 FT DISULFID 275 352 BY SIMILARITY.
 FT DISULFID 296 335 BY SIMILARITY.
 FT DISULFID 324 347 BY SIMILARITY.
 FT DISULFID 377 454 BY SIMILARITY.
 FT DISULFID 398 437 BY SIMILARITY.
 FT DISULFID 426 449 BY SIMILARITY.
 FT DISULFID 481 560 BY SIMILARITY.
 FT DISULFID 502 543 BY SIMILARITY.
 FT DISULFID 531 555 BY SIMILARITY.
 FT DISULFID 567 685 BY SIMILARITY.
 FT DISULFID 577 585 BY SIMILARITY.
 FT DISULFID 607 623 BY SIMILARITY.
 FT DISULFID 699 766 BY SIMILARITY.
 FT DISULFID 729 745 BY SIMILARITY.
 FT DISULFID 756 784 BY SIMILARITY.
 FT CARBOHD 365 365 O-LINKED (GLUCNA...) (BY SIMILARITY).
 SQ SEQUENCE 810 AA; 90255 MW; A75E1C51A0F24A CRC64;

Query Match 93.3%; Score 70; DB 1; Length 810;
 Best Local Similarity 100.0%; Pred. No. 0.00078;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNPDDGVGGPW 11
 |||||
 Db 532 RNPDDGVGGPW 542

RESULT 3
 PLNN_CANFA STANDARD; PRT; 333 AA.
 ID PLNN_CANFA

AC P80009; 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen (EC 3.4.21.7) (Fragment).
 GN PIG.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE:
 RC TISSUE-Plasma;
 RX MEDLINE=90175323; PubMed=2626424;
 RA Schaller J., Straub C., Kaempfer U., Rickli E.E.;
 RT "Complete amino acid sequence of canine miniplasminogen.";
 RL Protein Seq. Data Anal. 2:445-450(1985).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION: IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. ACTIVATED WITH UROKINASE AND HIGH CONCENTRATIONS OF
 CC STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS AT LEAST 1 KRINGLE DOMAIN.
 DR HSSP: P00747; 5HPG.
 DR MEROPS: S01.233;
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; kringle; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00020; TRYP_Spec; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR Hydroxylase: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen.
 FT NON_TER 1
 FT CHAIN <1 103 PLASMIN HEAVY CHAIN A.
 FT 333 104 333 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 4 83 KRINGLE 5.
 FT 104 333
 FT DISULFID 4 83 SERINE PROTEASE.
 FT DISULFID 25 66 BY SIMILARITY.
 FT DISULFID 54 78 BY SIMILARITY.
 FT DISULFID 90 208 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 100 108 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 130 146 BY SIMILARITY.
 FT DISULFID 222 289 BY SIMILARITY.
 FT DISULFID 252 268 BY SIMILARITY.
 FT DISULFID 279 307 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 145 145 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 188 188 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 283 283 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT SITE 152 152 STREPTOKINASE-BINDING SITE (PROBABLE).
 FT SITE 186 186 STREPTOKINASE-BINDING SITE (PROBABLE).
 FT SITE 264 264 STREPTOKINASE-BINDING SITE (PROBABLE).
 FT SITE 277 277 SITE OF SUBSTRATE SPECIFICITY (BY SIMILARITY).
 FT SEQUENCE 333 AA: 36678 MW: C8C0271B6C6AC8D4 CRC64;

Query Match 85.3%; Score 64; DB 1; Length 333;
 Best Local Similarity 90.9%; Pred. No. 0.003;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RNPDDVGGPW 11
 |||||
 DB 55 RNPDDVGGPW 65
 RESULT 4
 ID PLMN_HORSE STANDARD; PRT; 338 AA.
 AC P80010;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen (EC 3.4.21.7) (Fragment).
 GN PIG.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE:
 RC TISSUE-Plasma;
 RX MEDLINE=92052077; PubMed=1946332;
 RA Schaller J., Straub C., Kaempfer U., Rickli E.E.;
 RT "Complete amino acid sequence of equine miniplasminogen.";
 RL Protein Seq. Data Anal. 4:69-74(1991).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION: IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS AT LEAST 1 KRINGLE DOMAIN.
 DR HSP: S17527; S17527.
 DR HSP: P00747; 5HPG.
 DR MEROPS: S01.233;
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; kringle; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00020; TRYP_Spec; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR Hydroxylase: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen.
 FT NON_TER 1
 FT CHAIN <1 108 PLASMIN HEAVY CHAIN A.
 FT 333 109 338 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 9 88 KRINGLE 5.
 FT 109 338
 FT DISULFID 9 88 SERINE PROTEASE.
 FT DISULFID 30 88 BY SIMILARITY.
 FT DISULFID 71 71 BY SIMILARITY.
 FT DISULFID 59 83 BY SIMILARITY.
 FT DISULFID 95 213 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 105 113 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 135 151 BY SIMILARITY.
 FT DISULFID 227 294 BY SIMILARITY.

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FT DISULFID 257 273 BY SIMILARITY.
FT DISULFID 284 312 BY SIMILARITY.
FT ACT_SITE 150 150 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 193 193 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 288 288 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT SITE 157 157 STREPTOKINASE-BINDING SITE (PROBABLE).
FT SITE 191 191 STREPTOKINASE-BINDING SITE (PROBABLE).
FT SITE 269 269 STREPTOKINASE-BINDING SITE (PROBABLE).
FT SITE 282 282 SITE OF SUBSTRATE SPECIFICITY
      (BY SIMILARITY).
SQ SEQUENCE 338 AA; 37132 MW; 8E9E56B5C5CDBE01 CRC64;

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Query Match 85.3%; Score 64; DB 1; Length 338;
 Best Local Similarity 90.9%; Pred. No. 0.0031;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 RNPDDGVGCPW 11
   | | | | | | | |
Db 60 RNPDDGVNGPW 70

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RESULT 5
 PLMN_SHEEP STANDARD; PRT; 343 AA.
 ID PLMN_SHEEP
 AC P81286;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen (EC 3.4.21.7) (Fragment).
 GN Plg.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprine; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=9314995; PubMed=1492092;
 RX Schaller J., Straub C., Kamper U., Rickli E.F.;
 RT "Complete amino acid sequence of ovine miniplasminogen.";
 RL Protein Seq. Data Anal. 5:21-25(1992).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPsin FAMILY. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS AT LEAST 2 KRINGLE DOMAINS.
 DR HSP: P00747; 5HKG.
 DR MEROPS: S01.233.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; Kringle_1.
 DR Pfam: PF00089; trypsin; 1.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS00070; KRINGLE_2; 1.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen.
 FT NON_TER 1

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FT DOMAIN <1 140 HEAVY CHAIN A.
FT DOMAIN 141 >343 LIGHT CHAIN A.
FT DOMAIN <1 17 KRINGLE 4.
FT DOMAIN 41 120 KRINGLE 5.
FT DOMAIN 114 341 SERINE PROTEASE.
FT ACT_SITE 181 181 CHARGE RELAY SYSTEM.
FT ACT_SITE 224 224 CHARGE RELAY SYSTEM.
FT ACT_SITE 319 319 CHARGE RELAY SYSTEM.
FT NON_TER 343 343
SQ SEQUENCE 343 AA; 37662 MW; 8DF6EBA92D596EE0 CRC64;

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Query Match 85.3%; Score 64; DB 1; Length 343;
 Best Local Similarity 90.9%; Pred. No. 0.0031;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 RNPDDGVGCPW 11
   | | | | | | | |
Db 66 RNPDDGVNGPW 76

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RESULT 6
 HGFL_HUMAN STANDARD; PRT; 711 AA.
 ID HGFL_HUMAN
 AC P26927; Q13350; Q14870;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hepatocyte growth factor-like protein precursor (Macrophage
 DE stimulatory protein) (MSP) (Macrophage stimulating protein).
 GN MST1 OR HGFL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92002016; PubMed=1655021;
 RA Han S., Stuart L.A., Friesner Deegen S.J.;
 RT "Characterization of the DNF152 locus on human chromosome 3;
 RT identification of a gene coding for four kringle domains with
 RT homology to hepatocyte growth factor.";
 RL Biochemistry 30:9768-9780(1991).
 CC -1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
 CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
 CONSERVED.
 CC -1- PTM: MAY BE CLEAVED AFTER AA 484, TO YIELD A TWO-CHAIN MOLECULE
 HELD TOGETHER BY DISULFIDE BONDS, OR TWO SEPARATE POLYPEPTIDES.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPsin FAMILY. PLASMINOGEN SUBFAMILY.
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 or send an email to license@sib-sib.ch).
 DR EMBL: M4178; AAA50165.1;
 DR EMBL: U37055; AAC50471.1;
 DR EMBL: I11924; AAA59872.1;
 DR PIR: A40331; A40331.

DR HSP: P00747; 2PK4.
 DR MEROPS: S01.975; -.
 DR MIM: 142408; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan-app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; Kringle; 4.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00021; KRINGLE_1; 4.
 DR PROSITE: PS00070; KRINGLE_2; 4.
 DR PROSITE: PS0240; TRYPSIN_DOM; 1.
 DR Kringle; Glycoprotein; Serine protease homolog; Signal;
 KW polymorphism.
 FT SIGNAL 1 18
 FT CHAIN 19 711
 FT DOMAIN 32 109
 FT DOMAIN 110 186
 FT DOMAIN 191 268
 FT DOMAIN 283 361
 FT DOMAIN 370 448
 FT DOMAIN 484 711
 FT DISULFID 56 78
 FT DISULFID 60 66
 FT DISULFID 110 166
 FT DISULFID 131 159
 FT DISULFID 157 181
 FT DISULFID 191 268
 FT DISULFID 194 324
 FT DISULFID 212 251
 FT DISULFID 240 261
 FT DISULFID 283 361
 FT DISULFID 304 343
 FT DISULFID 332 355
 FT DISULFID 370 448
 FT DISULFID 391 431
 FT DISULFID 419 443
 FT DISULFID 468 588
 FT DISULFID 507 523
 FT DISULFID 602 667
 FT DISULFID 632 646
 FT DISULFID 657 685
 FT CARBOHYD 72 72
 FT CARBOHYD 296 296
 FT CARBOHYD 615 615
 FT VARIANT 13 13
 FT VARIANT
 FT VARIANT
 FT VARIANT
 FT CONFLICT 623 623
 FT SEQUENCE 711 AA; 80379 MW; 596ED21F180290E4 CRC64;
 Query Match 85.3%; Score 64; DB 1; Length 711;
 Best Local Similarity 90.9%; Pred. No. 0.0065;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7
 PLIN BOVIN STANDARD; PRT; 812 AA.
 AC P06868; 028162;
 DT 01-JAN-1988 (Rel. 06, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7).
 GN PLG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Berglund L., Andersen M.D., Petersen T.E.;
 RT "Cloning and characterization of the bovine plasminogen cDNA";
 RL Int. Dairy J. 5:593-603(1995).
 RN [2]
 RP SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=85203906; PubMed=3846532;
 RA Schaller J., Moser P.W., Danneberg-Muller G.A.K., Rosselet S.J.,
 RA Kamfer U., Rickli E.E.;
 RT "Complete amino acid sequence of bovine plasminogen. Comparison with
 human plasminogen";
 RL Eur. J. Biochem. 149:267-278(1985).
 RN [3]
 RP SEQUENCE OF 706-812 FROM N.A.
 RX MEDLINE=85023311; PubMed=6148961;
 RA Malinowski D.P., Sadler J.E., Davie E.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 human and bovine plasminogen";
 RL Biochemistry 23:4243-4250(1984).
 RN [4]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamberling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 plasminogen. Species specificity in relation to sialylation and
 fucosylation patterns";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5, IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- PTM: N-LINKED GLYCAN CONTAIN N-ACETYLGLUCOSAMINE AND SULFIC ACID.
 CC O-LINKED GLYCANS CONSIST OF GAL-GALNAc DISACCHARIDE WITH IS
 MODIFIED WITH UP TO 2 SULFIC ACID RESIDUES (MICROHETEROGENEITY).
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPsin FAMILY. PLASMINOGEN SUBFAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL, X79402; CAAS5939.1; -;
 CC EMBL, K02935; AAA30714.1; -;
 CC PIR, A25835; PLBO.
 CC HSP: P00747; 2PK4.
 CC MEROPS: S01.233; -;
 CC GlycoSuiteDB: P06868; -;

DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; Kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRYOTRYPSIN.
 DR SMART: SM00130; KR; 5.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; TRY_SPE; 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS00070; KRINGLE_2; 5.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydrolase: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KM Tissue remodeling; Blood coagulation; Kringle; zymogen; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 812 PLASMINOGEN.
 FT CHAIN 27 583 PLASMIN HEAVY CHAIN A.
 FT CHAIN 584 812 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 110 188 KRINGLE 1.
 FT DOMAIN 192 269 KRINGLE 2.
 FT DOMAIN 282 359 KRINGLE 3.
 FT DOMAIN 384 461 KRINGLE 4.
 FT DOMAIN 485 564 KRINGLE 5.
 FT DOMAIN 584 812 SERINE PROTEASE.
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 365 365 FTID-CAR_000014.
 FT CARBOHYD 365 365 O-LINKED (GALNAC. . .).
 FT ACT_SITE 624 624 CHARGE RELAY SYSTEM.
 FT ACT_SITE 667 667 CHARGE RELAY SYSTEM.
 FT ACT_SITE 762 762 CHANGE RELAY SYSTEM.
 FT CONFLICT 335 335 N -> D (IN REF. 2).
 FT CONFLICT 516 516 O -> H (IN REF. 2).
 FT CONFLICT 555 555 P -> L (IN REF. 2).
 FT CONFLICT 744 744 T -> R (IN REF. 3).
 SQ SEQUENCE 812 AA; 91216 MW; 38A6AA691E220946 CRC64;

Query Match 85.3%; Score 64; DB 1; Length 812;
 Best Local Similarity 90.9%; Pred. No. 0.0075;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNPDSGVGSPW 11
 |||||
 DB 536 RNPDSGVGSPW 546

RESULT 8
 PLMN_MOUSE STANDARD; PRT; 812 AA.
 ID P20918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
 GN Plg.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91184812; PubMed=2081600;
 RA Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
 RT "Characterization of the cDNA coding for mouse plasminogen and
 RT localization of the gene to mouse chromosome 17.";
 RL Genomics 8:49-61(1990).
 FT [2]

RP CHARACTERIZATION OF ANGIOSTATIN AND PARTIAL SEQUENCE.
 RX MEDLINE=95042728; PubMed=7525077;
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
 RT suppression of metastases by a Lewis lung carcinoma.";
 RL Cell 79:315-328(1994).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
 CC NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
 CC METASTATIC TUMORS IN VIVO.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
 CC INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD
 CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
 CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: J04766; AAA50168.1; -.
 DR PIR: A38514; A38514.
 DR HSSP: P00747; LPMK.
 DR MEROPS: S01.233; -.
 DR MGD: MGI:97620; Plg.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; Kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRYOTRYPSIN.
 DR SMART: SM00130; KR; 5.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; TRY_SPE; 1.
 DR PROSITE: PS00021; KRINGLE_1; 4.
 DR PROSITE: PS00070; KRINGLE_2; 5.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydrolase: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; zymogen; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 812 PLASMINOGEN.
 FT CHAIN 20 581 PLASMIN HEAVY CHAIN A.
 FT PEPTIDE 20 97 ACTIVATION PEPTIDE.
 FT CHAIN 98 581 PLASMIN SHORT FORM OF CHAIN A.
 FT CHAIN 98 7436 ANGIOSTATIN.
 FT CHAIN 582 812 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 103 181 KRINGLE 1.
 FT DOMAIN 184 262 KRINGLE 2.

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FT DOMAIN 275 352 KRINGLE 3.
FT DOMAIN 377 454 KRINGLE 4.
FT DOMAIN 481 560 KRINGLE 5.
FT DOMAIN 582 812 SERINE PROTEASE.
FT ACT_SITE 624 624 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 667 667 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 762 762 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 49 73 BY SIMILARITY.
FT DISULFID 53 61 BY SIMILARITY.
FT DISULFID 103 181 BY SIMILARITY.
FT DISULFID 124 164 BY SIMILARITY.
FT DISULFID 132 176 BY SIMILARITY.
FT DISULFID 185 262 BY SIMILARITY.
FT DISULFID 188 316 BY SIMILARITY.
FT DISULFID 206 245 BY SIMILARITY.
FT DISULFID 234 257 BY SIMILARITY.
FT DISULFID 275 352 BY SIMILARITY.
FT DISULFID 296 335 BY SIMILARITY.
FT DISULFID 324 347 BY SIMILARITY.
FT DISULFID 377 454 BY SIMILARITY.
FT DISULFID 398 437 BY SIMILARITY.
FT DISULFID 426 449 BY SIMILARITY.
FT DISULFID 481 560 BY SIMILARITY.
FT DISULFID 502 543 BY SIMILARITY.
FT DISULFID 531 555 BY SIMILARITY.
FT DISULFID 568 687 INTERCHAIN (BY SIMILARITY).
FT DISULFID 578 586 INTERCHAIN (BY SIMILARITY).
FT DISULFID 609 625 BY SIMILARITY.
FT DISULFID 701 768 BY SIMILARITY.
FT DISULFID 731 747 BY SIMILARITY.
FT DISULFID 758 786 BY SIMILARITY.
SQ SEQUENCE 812 AA; 90846 MW; D34A74A4FC2256F8 CRC64;

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Query Match 85.3%; Score 64; DB 1; Length 812;
Best Local Similarity 90.9%; Pred No. 0.0075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 RNPDPGVGGPW 11
DB 532 RNPDPGVGGPW 542

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RESULT 9
APOA_HUMAN STANDARD; PRT; 4548 AA.

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AC APOA_HUMAN 008519;
AD 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Apolipoprotein(a) precursor (BC 3.4.21.-) (Apo(a)) (Lp(a)).
GN LpA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=88039109; PubMed=3670400;
RA McLean J.W., Tomlison J.E., Kuang W.-J., Eaton D.L., Chen E.Y.,
RA Fless G.M., Scanu A.M., Lawn R.M.;
RA "cDNA sequence of human apolipoprotein(a) is homologous to
RT plasminogen."
RL Nature 330:132-137(1987).
RN 12
RP SERINE PROTEASE ACTIVITY.
RX MEDLINE=90076123; PubMed=2531657;
RA Salonen E.-M., Jauhainen M., Zardi L., Vaheri A., Ehnholm C.;
RA "Lipoprotein(a) binds to fibrinogen and has serine proteinase
RT activity capable of cleaving it."
RL EMBO J. 8:4035-4040(1989).
RN 13
RP REVIEW.
RX MEDLINE=90049223; PubMed=2530631;

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RA Utermann G.;
RT "The mysteries of lipoprotein(a).";
RL Science 246:904-910(1989).
RN 14
RP CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.
RX MEDLINE=21303595; PubMed=11294842;
RA Garner B., Merry A.H., Royle L., Harvey D.J., Rudd P.M., Thillet J.;
RT "Structural elucidation of the N- and O-glycans of human
RT apolipoprotein(a): role of O-glycans in conferring protease
RT resistance."
RL J. Biol. Chem. 276:22200-22208(2001).
RN 15
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.
RX MEDLINE=96217891; PubMed=8642595;
RA Mikol V., Loggrosso P.V., Boettcher B.R.;
RT "Crystal structures of apolipoprotein(a) kringle IV37 free and
RT complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic
RT acid: existence of novel and expected binding modes."
RL J. Mol. Biol. 256:751-761(1996).
RN 16
RP VARIANT ARG-4193.
RX MEDLINE=95002201; PubMed=7918682;
RA Scanu A.M., Pfaffinger D., Lee J.C., Himan J.;
RT "A single point mutation (Trp72->Arg) in human apo(a) kringle 4-37
RT associated with a lysine binding defect in Lp(a).";
RL Biochim. Biophys. Acta 1227:41-45(1994).
CC 1- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
CC (Lp(a)). It has serine proteinase activity and is able of
CC autoproteolysis. Inhibits tissue-type plasminogen activator 1.
CC Lp(a) may be a ligand for megalin/Gp 330.
CC 1- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibrinogen and
CC decorin.
CC 1- PTM: N- and O-glycosylated. The N-glycans are complex biantennary
CC structures present in either a mono- or disialylated state. The
CC O-glycans are mostly (80%) represented by the monosialylated core
CC type I structure, NeuNacalpa2-3Galbeta1-3GalNAc, with smaller
CC amounts of disialylated and non-sialylated O-glycans also
CC detected.
CC 1- DISEASE: Elevated plasma concentrations of apo(a) and its
CC naturally occurring proteolytic fragments is correlated with
CC atherosclerosis. Homology with plasminogen kringle IV and V is
CC thought to underlie the atherogenicity of the protein, because the
CC fragments are competing with plasminogen for fibrin(ogen) binding.
CC 1- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
CC leading to the formation of the so called mini-Lp(a). Apo(a)
CC fragments accumulate in atherosclerotic lesions, where they may
CC promote thrombogenesis. O-glycosylation may limit the extent of
CC proteolytic fragmentation.
CC 1- SIMILARITY: CONTAINS 38 KRINGLE DOMAINS.
CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
CC -----
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CC -----
DR EMBL; X06290; CAA29618.1; -
DR PIR; S00657; S00657.
DR HSSP; P00747; 1PMK.
DR MR0PS; S01.226; -.
DR MTM; 152200; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Trypsin.
DR Pfam; PF00051; kringle; 38.
DR PRINTS; PR00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR SMART; SM00130; KR; 38.

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DR SMART: SM00020: Tryp.Spc: 1.
 DR PROSITE: PS00021: KRINGLE_1; 38.
 DR PROSITE: PS50070: KRINGLE_2; 38.
 DR PROSITE: PS50240: TRYPSIN_DOM; 1.
 DR PROSITE: PS00134: TRYPSIN_HIS; 1.
 DR PROSITE: PS00135: TRYPSIN_SER; 1.
 DR Hydrolase: Serine protease; Lipid transport; Plasma; Glycoprotein;
 KR Kringle; Repeat; Atherosclerosis; Signal; Polymorphism.
 KM SIGNAL: 1 19
 FT CHAIN 20 4548 APOLOPROTEIN(A).
 FT DOMAIN 20 130 KRINGLE TYPE IV, 1.
 FT DOMAIN 131 244 KRINGLE TYPE IV, 2.
 FT DOMAIN 245 358 KRINGLE TYPE IV, 3.
 FT DOMAIN 359 472 KRINGLE TYPE IV, 4.
 FT DOMAIN 473 586 KRINGLE TYPE IV, 5.
 FT DOMAIN 587 700 KRINGLE TYPE IV, 6.
 FT DOMAIN 701 814 KRINGLE TYPE IV, 7.
 FT DOMAIN 815 928 KRINGLE TYPE IV, 8.
 FT DOMAIN 929 1042 KRINGLE TYPE IV, 9.
 FT DOMAIN 1043 1156 KRINGLE TYPE IV, 10.
 FT DOMAIN 1157 1270 KRINGLE TYPE IV, 11.
 FT DOMAIN 1271 1384 KRINGLE TYPE IV, 12.
 FT DOMAIN 1385 1498 KRINGLE TYPE IV, 13.
 FT DOMAIN 1499 1612 KRINGLE TYPE IV, 14.
 FT DOMAIN 1613 1726 KRINGLE TYPE IV, 15.
 FT DOMAIN 1727 1840 KRINGLE TYPE IV, 16.
 FT DOMAIN 1841 1954 KRINGLE TYPE IV, 17.
 FT DOMAIN 1955 2068 KRINGLE TYPE IV, 18.
 FT DOMAIN 2069 2182 KRINGLE TYPE IV, 19.
 FT DOMAIN 2183 2296 KRINGLE TYPE IV, 20.
 FT DOMAIN 2297 2410 KRINGLE TYPE IV, 21.
 FT DOMAIN 2411 2524 KRINGLE TYPE IV, 22.
 FT DOMAIN 2525 2638 KRINGLE TYPE IV, 23.
 FT DOMAIN 2639 2752 KRINGLE TYPE IV, 24.
 FT DOMAIN 2753 2866 KRINGLE TYPE IV, 25.
 FT DOMAIN 2867 2980 KRINGLE TYPE IV, 26.
 FT DOMAIN 2981 3094 KRINGLE TYPE IV, 27.
 FT DOMAIN 3095 3208 KRINGLE TYPE IV, 28.
 FT DOMAIN 3209 3322 KRINGLE TYPE IV, 29.
 FT DOMAIN 3323 3436 KRINGLE TYPE IV, 30.
 FT DOMAIN 3437 3550 KRINGLE TYPE IV, 31.
 FT DOMAIN 3551 3664 KRINGLE TYPE IV, 32.
 FT DOMAIN 3665 3777 KRINGLE TYPE IV, 33.
 FT DOMAIN 3778 3891 KRINGLE TYPE IV, 34.
 FT DOMAIN 3892 4005 KRINGLE TYPE IV, 35.
 FT DOMAIN 4006 4119 KRINGLE TYPE IV, 36.
 FT DOMAIN 4120 4233 KRINGLE TYPE IV, 37.
 FT DOMAIN 4234 4347 KRINGLE TYPE IV, 38.
 FT DOMAIN 4348 4461 KRINGLE TYPE IV, 39.
 FT ACT_SITE 4462 4575 CHARGE RELAY SYSTEM.
 FT ACT_SITE 4576 4689 CHARGE RELAY SYSTEM.
 FT ACT_SITE 4690 4803 CHARGE RELAY SYSTEM.
 FT ACT_SITE 4804 4917 CHARGE RELAY SYSTEM.
 FT VARIANT 4918 5031 W -> R (LOSS OF LYSINE-SEPAPHOROSE BINDING).
 FT SEQUENCE 4548 AA: 501313 MW: 96921BES6A465C5F CRC64;
 FT FTID-VAR:006633.
 Query Match 84.0%; Score 63; DB 1; Length 4548;
 Best Local Similarity 81.8%; Pred. No. 0.063;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DE Plasminogen precursor (EC 3.4.21.7).
 GN pig.
 OS *Ericaceae europaeus* (Western European hedgehog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
 OC NCBI_TaxID=9365;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=liver;
 RA MEDLINE=96025778; PubMed=7592597;
 RX Lawn R.M., Boomgard N.W., Schwartz K., Lindahl G.E., Wade D.P.,
 RA Byrne C.D., Fong K.J., Meer K., Pally L.;
 RT "The recurring evolution of lipoprotein(a). Insights from cloning of
 RL hedgehog apolipoprotein(a).";
 RN J Biol. Chem. 270:24004-24009(1995).
 RP REVISIONS.
 RA Lawn R.M.;
 RL submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE OKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY
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 CC
 CC EMBL: U33171; AAC48717.1; -;
 CC HSSP: P00747; IPWK.
 CC MEROPS: S01.233; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; PAN_app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; Kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 5.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020: Tryp.Spc: 1.
 DR PROSITE: PS00021: KRINGLE_1; 5.
 DR PROSITE: PS50070: KRINGLE_2; 5.
 DR PROSITE: PS50240: TRYPSIN_DOM; 1.
 DR PROSITE: PS00134: TRYPSIN_HIS; 1.
 DR PROSITE: PS00135: TRYPSIN_SER; 1.
 DR Hydrolase: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KM Tissue remodeling; Blood coagulation; Kringle; Zymogen; Signal.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 810 PLASMINOGEN.
 FT CHAIN 20 582 PLASMIN HEAVY CHAIN A (BY SIMILARITY).
 FT CHAIN 583 810 PLASMIN LIGHT CHAIN B (BY SIMILARITY).
 FT DOMAIN 103 181 KRINGLE 1.

FT DOMAIN 185 262 KRINGLE 2.
 FT DOMAIN 275 352 KRINGLE 3.
 FT DOMAIN 379 456 KRINGLE 4.
 FT DOMAIN 482 561 KRINGLE 5.
 FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
 FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
 FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
 FT CARBOHYD 339 339 N-LINKED (GICMNC...) (POTENTIAL).
 SO SEQUENCE 810 AA: 90902 MW: 8E5780946017A16 CRC64;

Query Match 80.0%; Score 60; DB 1; Length 810;
 Best Local Similarity 81.8%; Pred. No. 0.033;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 533 RNDPDDVGGPW 543

RESULT 11
 ID PLMN_PIG STANDARD: PRT: 790 AA.
 AC P06867:
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasmimogen (EC 3.4.21.7).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE OF 1-560.
 RA Schaller J., Marti T., Roesselet S.J., Kaempfer U., Rickli E.F.;
 RT "Amino acid sequence of the heavy chain of porcine plasmin. Comparison
 of the carbohydrate attachment sites with the human and bovine
 species.";
 RL Fidinolysis 1:91-102(1987).
 RN [2]
 RP SEQUENCE OF 450-790.
 RX MEDLINE=85203907; PubMed=3846533;
 RA Marti T., Schaller J., Rickli E.F.;
 RT "Determination of the complete amino-acid sequence of porcine
 multiplasminogen.";
 RL Eur. J. Biochem. 149:279-285(1985).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.F., Schmid K., Kamerling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 plasminogen. Species specificity in relation to sterylolation and
 fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- PTM: N-LINKED GLYCAN CONTAINS N-ACETYLGLUCOSAMINE, SIALIC ACID AND
 IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAc
 DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
 (MICROHETEROGENEITY).
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC -1- IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

CC TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
 DR PIR: A25834; A25834.
 DR PIR: S03733; S03733.
 DR HSSD: P00747; SHPG.
 DR MEROPS: S01.233; -;
 DR GlycoSiteDB: P06867; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003609; Pan-app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF000251; Kringle_5.
 DR Pfam: PF00024; Pan_1.
 DR Pfam: PF00089; Trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR_5.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS00070; KRINGLE_2; 5.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Plasmin heavy chain A.
 FT CHAIN 1 560 PLASMIN LIGHT CHAIN B.
 FT CHAIN 561 790 SERINE PROTEASE.
 FT DOMAIN 561 790 KRINGLE 1.
 FT DOMAIN 84 162 KRINGLE 1.
 FT DOMAIN 166 243 KRINGLE 2.
 FT DOMAIN 256 333 KRINGLE 3.
 FT DOMAIN 358 435 KRINGLE 4.
 FT DOMAIN 461 540 KRINGLE 5.
 FT ACT_SITE 602 602 CHARGE RELAY SYSTEM.
 FT ACT_SITE 645 645 CHARGE RELAY SYSTEM.
 FT ACT_SITE 740 740 CHARGE RELAY SYSTEM.
 FT CARBOHYD 289 289 N-LINKED (GICMNC...).
 FT CARBOHYD 340 340 /FTID=CAR_000019.
 FT SEQUENCE 790 AA: 88592 MW: F04EA06E74BCD58E CRC64;
 SO

Query Match 76.0%; Score 57; DB 1; Length 790;
 Best Local Similarity 81.8%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 512 RNDPDDVGGPW 522

RESULT 12
 ID HGFL_MOUSE STANDARD: PRT: 716 AA.
 AC P26928:
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hepatocyte growth factor-like protein precursor (Macrophage
 stimulatory protein) (MSP).
 DE Mst1 or HGFL.
 GN Mst1 or HGFL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Liver;
 RX MEDLINE=92002017; PubMed=1832957;
 RA Friesner Degen S.J., Stuart L.A., Han S., Jamison C.S.;
 RT "Characterization of the mouse cDNA and gene coding for a hepatocyte
 growth factor-like protein: expression during development.";

Biochemistry 30:9781-9791(1991).
 CC -1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
 CC CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
 CC CONSERVED.
 CC -1- TISSUE SPECIFICITY: LIVER, LOWER LEVELS IN LUNG, PLACENTA AND
 CC ADRENAL.
 CC -1- DEVELOPMENTAL STAGE: IS EXPRESSED AT LOW LEVELS DURING GESTATION.
 CC JUST BEFORE BIRTH THE LEVEL INCREASES DRAMATICALLY AND REMAINS
 CC STABLE AFTERWARDS.
 CC -1- P1N: MAY BE CLEAVED AFTER AA 488, TO YIELD A TWO-CHAIN MOLECULE
 CC HELD TOGETHER BY DISULFIDE BONDS, OR CLEAVED INTO TWO SEPARATE
 CC POLYPEPTIDES.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.

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 CC EMBL: M74180; AAA50166.1; -;
 CC EMBL: M74181; AAA50167.1; -;
 CC HSSP: P00747; ICRN.
 CC MEROPS: S01.975; -;
 CC MGD: MGI:96080; Hg1.
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR000001; Kringle.
 CC InterPro: IPR003014; PAN.
 CC InterPro: IPR003609; Pan_app.
 CC InterPro: IPR001254; Trypsin.
 CC Pfam: PF00051; Kringle; 4.
 CC Pfam: PF00024; PAN; 1.
 CC Pfam: PF00089; trypsin; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00018; KRINGLE.
 CC SMART: SM00130; KR; 4.
 CC SMART: SM00473; PAN_AP; 1.
 CC SMART: SM00020; TRYP_SPE; 1.
 CC PROSITE: PS00021; KRINGLE_1; 4.
 CC PROSITE: PS00070; KRINGLE_2; 4.
 CC PROSITE: PS00240; TRYPSIN_DOM; 1.
 CC Kringler: Glycoprotein, Serine protease homolog; Signal.
 CC SIGNAL 1 18
 CC CHAIN 19 716
 CC DOMAIN 19 109
 CC DOMAIN 110 186
 CC DOMAIN 191 268
 CC DOMAIN 292 370
 CC DOMAIN 379 457
 CC DOMAIN 489 716
 CC DISULFID 56 78
 CC DISULFID 60 66
 CC DISULFID 110 186
 CC DISULFID 131 169
 CC DISULFID 157 181
 CC DISULFID 191 268
 CC DISULFID 194 333
 CC DISULFID 212 251
 CC DISULFID 240 263
 CC DISULFID 292 370
 CC DISULFID 313 352
 CC DISULFID 341 364
 CC DISULFID 379 457
 CC DISULFID 400 440
 CC DISULFID 428 452
 CC DISULFID 477 593
 CC DISULFID 512 528
 CC DISULFID 607 651
 CC DISULFID 637 651
 CC POTENTIAL.
 CC HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.
 CC PAP.
 CC KRINGLE 1.
 CC KRINGLE 2.
 CC KRINGLE 3.
 CC KRINGLE 4.
 CC SERINE PROTEASE-LIKE.

PT DISULFID 662 690 BY SIMILARITY.
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 19 19 P -> Q (IN GENOMIC SEQUENCE).
 SO SEQUENCE 716 AA; 80588 MW; BBCE02FE85213ACC CRC64;
 Query Match 74.7%; Score 56; DB 1; Length 716;
 Best Local Similarity 81.8%; Fred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 RNPBGVGPW 11
 Db 429 RNPBGDSHCPW 439
 ||||| |||
 RESULT 13
 THRB_BOVIN STANDARD; PRT; 625 AA.
 ID THRB_BOVIN
 AC P00735;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_Taxid:9913;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88245190; PubMed-3379642;
 RA Irwin D.M., Robertson K.A., Macgillivray R.T.A.;
 RT "Structure and evolution of the bovine prothrombin gene";
 RL J. Mol. Biol. 200;31-45(1988).
 RN 12
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84203525; PubMed-6326805;
 RA McGillivray R.T.A., Davie E.W.;
 RT "Characterization of bovine prothrombin mRNA and its translation
 RT product";
 RL Biochemistry 23:1626-1634(1984).
 RN 13
 RP SEQUENCE OF 44-625. DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RA Magnusson S., Soltrop-Jensen L., Petersen T.E., Claess H.;
 RL (in) Hemker H.C., Velikamp J.J. (eds.);
 RL Boerhaave symposium on prothrombin and related coagulation factors,
 RL pp.25-46, Leiden University Press, Leiden (1975).
 RN 14
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 RX MEDLINE-86296631; PubMed-3741841;
 RA Park C.H., Tulinsky A.;
 RT "Three-dimensional structure of the kringle sequence: structure of
 RT prothrombin fragment 1";
 RL Biochemistry 25:3977-3982(1986).
 RN 15
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 RX MEDLINE-91311686; PubMed-1856869;
 RA Seshadri T.-P., Tulinsky A., Skrzypczak-Jankun E., Park C.H.;
 RT "Structure of bovine prothrombin fragment 1 refined at 2.25-A
 RT resolution";
 RL J. Mol. Biol. 220:481-494(1991).
 RN 16
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 RX MEDLINE-92190185; PubMed-1547238;
 RA Soriano-Garcia M., Padmanabhan K., de Vos A.M., Tulinsky A.;
 RT "The Ca2+ ion and membrane binding structure of the Gla domain of Ca-
 RT prothrombin fragment 1";
 RL Biochemistry 31:2554-2566(1992).
 RN 17
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

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RA MEDLINE:92218459; PubMed=1560020;
RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
RT "The structure of residues 7-16 of the A alpha chain of human
RT fibrinogen bound to bovine thrombin at 2.3-A resolution.";
RL J. Biol. Chem. 267:7911-7920(1992).
RN
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=92389319; PubMed=1518046;
RA Brandstetter H., Turk D., Hoeffken H.W., Grosse D., Stuerzbecher J.,
RA Martin P.D., Edwards B.F.P., Bode W.;
RT "Refined 2.3 A X-ray crystal structure of bovine thrombin complexes
RT formed with the benzamidine and arginine-based thrombin inhibitors
RT NAPAP, 4-TAPAP and MOPAP. A starting point for improving
RT antithrombotics.";
RL J. Mol. Biol. 226:1085-1089(1992).
RN
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.
RX MEDLINE=97102783; PubMed=8947023;
RA van de Loch A., Stubbs M.T., Bode W., Friedrich T., Bollschweiler C.,
RA Hoeffken W., Huber R.;
RT "The ornithodorin-thrombin crystal structure, a key to the TAP
RT enigma?";
RL EMBO J. 15:6011-6017(1996).
RN
RP [10]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIBLIN.
RX MEDLINE=98004486; PubMed=934235;
RA Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schlenning W.D.,
RA Huber R., Bode W.;
RT "Structure of the thrombin complex with triblin, a lipocalin-like
RT exosite-binding inhibitor derived from a triatomine bug.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
RN
RP [11]
RX GENE STRUCTURE.
RX MEDLINE=96077733; PubMed=3000440;
RA Irwin D.M., Ahern K.G., Pearson G.D., McGillivray R.T.A.;
RT "Characterization of the bovine prothrombin gene.";
RL Biochemistry 24:6854-6861(1985).
RN
RP -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
RN FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
RN AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
RN -1- SUBCELLULAR LOCATION: extracellular.
RN -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER. FOUND IN PLASMA.
RN -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
RN RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOAL
RN ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
RN ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
RN CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
RN OF PROTHROMBIN TO THROMBIN.
RN -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
RN PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
RN FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
RN THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
RN HEAVY CHAINS. THE ACTIVATION PROCESS SLOWLY BECAUSE FACTOR
RN V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
RN THROMBIN.
RN -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
RN FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
RN BY FACTOR XA.
RN -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
RN -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
RN TRYPSIN FAMILY.
RN -1- DATABASE: NAME-Prozyme technical fact sheet;
RN WWW="http://www.prozyme.com/technical/thrombindata.html".
RN
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RN EMBL: V00135; CAA23451.1; -.

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DR	EMBL: J00041; AAA30781.1; .	
DR	PIR: A00915; TBBO	
DR	PIR: S02537; S02537.	
DR	PDB: 1BBR; 31-JAN-94.	
DR	PDB: 1EBR; 31-JAN-94.	
DR	PDB: 1ETS; 31-JAN-94.	
DR	PDB: 1ETT; 31-JAN-94.	
DR	PDB: 1HRT; 31-JAN-94.	
DR	PDB: 2PE1; 31-JAN-94.	
DR	PDB: 2PF2; 31-JAN-94.	
DR	PDB: 2SPT; 31-MAY-94.	
DR	PDB: 1MKW; 07-JUL-97.	
DR	PDB: 1IMX; 07-JUL-97.	
DR	PDB: 1TBO; 14-OCT-96.	
DR	PDB: 1TBR; 14-OCT-96.	
DR	PDB: 1TOC; 23-JUL-97.	
DR	PDB: 1VIT; 21-APR-97.	
DR	PDB: 1YCP; 06-MAY-98.	
DR	PDB: 1A0H; 17-JUN-98.	
DR	PDB: 1AVG; 16-FEB-99.	
DR	MEROPS: S01_217; .	
DR	InterPro: IPR001314; Chymotrypsin.	
DR	InterPro: IPR002383; GLA.Blood.	
DR	InterPro: IPR000001; Kringle.	
DR	InterPro: IPR003966; Prothrombin.	
DR	InterPro: IPR001254; Trypsin.	
DR	InterPro: IPR000294; Vtk_dep_GLA.	
DR	Pfam: PF00594; gla; 1.	
DR	Pfam: PF00051; kringle; 2.	
DR	Pfam: PF00089; trypsin; 1.	
DR	PRINTS: PR00722; CHYMOTRYPSIN.	
DR	PRINTS: PR00001; GLABLOOD.	
DR	PRINTS: PR00018; KRINGLE.	
DR	PRINTS: PR01505; PROTHROMBIN.	
DR	SMART: SM00069; GLA: 1.	
DR	SMART: SM00020; KR: 2.	
DR	SMART: SM00020; tryp_spec; 1.	
DR	PROSITE: PS00011; GLU_CARBOXYLATION; 1.	
DR	PROSITE: PS00021; KRINGLE_1; 2.	
DR	PROSITE: PS00070; KRINGLE_2; 2.	
DR	PROSITE: PS00240; TRYPSIN_DOM; 1.	
DR	PROSITE: PS00134; TRYPSIN_HTS; 1.	
DR	PROSITE: PS00135; TRYPSIN_SER; 1.	
KW	Blood coagulation; Plasma; calcium-binding; Glycoprotein; Repeat;	
KW	Vitamin K; zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver	
KW	Hydrolyase; Serine protease; Kringle; Signal; 3D-structure.	
FT	SIGNAL	1 24
FT	PROPEP	25 43
FT	CHAIN	44 625
FT	PEPTIDE	44 199
FT	PEPTIDE	200 317
FT	CHAIN	318 366
FT	CHAIN	367 625
FT	DOMAIN	109 187
FT	DOMAIN	214 292
FT	DOMAIN	367 625
FT	SITE	199 200
FT	SITE	317 318
FT	SITE	366 367
FT	ACT_SITE	409 409
FT	ACT_SITE	465 465
FT	ACT_SITE	571 571
FT	MOD_RES	50 50
FT	MOD_RES	51 51
FT	MOD_RES	58 58
FT	MOD_RES	60 60
FT	MOD_RES	63 63
FT	MOD_RES	64 64
FT	MOD_RES	69 69
FT	MOD_RES	70 70
FT	MOD_RES	73 73
FT	MOD_RES	76 76
FT	CARBOHYD	120 120

Query Match 73.3%; Score 55; DB 1; Length 625;
 Best Local Similarity 72.7%; Pred. No. 0.17;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNPDPVGGPW 11
 ||||| : |||
 Db 159 RNPDPGSGTGPW 169

RESULT 14
 HGF_HUMAN STANDARD; PRT; 728 AA.
 AC P14210; Q9UDU6; Q9BYL9;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hepatocyte growth factor precursor (scatter factor) (SF)
 DE (Hepatopoietin A).
 GN HGF OR HPTA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91340155; PubMed=1831432;
 RA Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;
 RT "Organization of the human hepatocyte growth factor-encoding gene";
 RL Gene 102:213-219(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=89392017; PubMed=2528952;
 RA Miyazawa K., Tsubouchi H., Naka D., Takahashi K., Okigaki M.,
 RA Arakaki N., Nakayama H., Hiroo S., Sakiyama O., Takahashi K.,
 RA Gohda E., Daikuhara Y., Kitamura N.;
 RT "Molecular cloning and sequence analysis of cDNA for human hepatocyte
 growth factor";
 RL Biochem. Biophys. Res. Commun. 163:967-973(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=91025062; PubMed=2145836;
 RA Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa T.,
 RA Asami O., Hagiya M., Nakamura T., Shimizu S.;
 RT "Isolation and expression of cDNA for different forms of hepatocyte
 growth factor from human leukocyte";
 RL Biochem. Biophys. Res. Commun. 172:321-327(1990).
 RN [4]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 55-73 AND 495-520.
 RC TISSUE=Liver;
 RX MEDLINE=90066676; PubMed=2531289;
 RA Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimonishi M.,
 RA Sugimura A., Tashiro K., Shimizu S.;
 RT "Molecular cloning and expression of human hepatocyte growth factor";
 RL Nature 342:440-443(1989).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic fibroblast;
 RX MEDLINE=91334393; PubMed=181266;
 RA Weider K.M., Arakaki N., Hartmann G., Vandekerckhove J., Weingart S.,
 RA Rieder H., Fontsch C., Tsubouchi H., Hishida T., Daikuhara Y.,
 RA Birmeier W.;
 RT "Evidence for the identity of human scatter factor and human
 hepatocyte growth factor";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005(1991).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Courtney L., Elliott G., Angell S.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 249-695 FROM N.A.

RX MEDLINE=91369928; PubMed=1832556;
 RA Miyazawa K., Kitamura A., Kitamura N.;
 RT "Structural organization and the transcription initiation site of the
 human hepatocyte growth factor gene";
 RL Biochemistry 30:9170-9176(1991).
 RN [8]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=91207365; PubMed=1826837;
 RA Yoshiyama Y., Arakaki N., Naka D., Takahashi K., Hiroo S., Kondo J.,
 RA Nakayama H., Gohda E., Kitamura N., Tsubouchi H., Ishii T.,
 RA Hishida T., Daikuhara Y.;
 RT "Identification of the N-terminal residue of the heavy chain of both
 native and recombinant human hepatocyte growth factor";
 RL Biochem. Biophys. Res. Commun. 175:660-667(1991).
 RN [9]
 RP CARBOHYDRATE-LINKAGE SITE 476.
 RX MEDLINE=93129192; PubMed=1482348;
 RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
 RA Nakamura T., Shimizu S.;
 RT "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
 on the alpha chain";
 RL Biochem. Biophys. Res. Commun. 189:1329-1335(1992).
 RN [10]
 RP MUTAGENESIS.
 RX MEDLINE=92331602; PubMed=1321034;
 RA Lokker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins K.A.,
 RA Baker J.B., Godowski P.J.;
 RT "Structure-function analysis of hepatocyte growth factor:
 identification of variants that lack mitogenic activity yet retain
 high affinity receptor binding";
 RL EMBO J. 11:2503-2510(1992).
 RN [11]
 RP STRUCTURE BY NMR OF 31-127
 RX MEDLINE=96154323; PubMed=9493272;
 RA Zhou H., Mazzulla M.J., Kaufman J.D., Stahl S.J., Wingfield P.T.,
 RA Rubin J.S., Bottaro D.P., Byrd R.A.;
 RT "The solution structure of the N-terminal domain of hepatocyte growth
 factor reveals a potential heparin-binding site";
 RL Structure 6:109-116(1998).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.
 RX MEDLINE=99036858; PubMed=9817840;
 RA Ulsch M., Lokker N.A., Godowski P.J., de Vos A.M.;
 RT "Crystal structure of the NK1 fragment of human hepatocyte growth
 factor at 2.0-A resolution";
 RL Structure 6:1383-1393(1998).
 CC -I- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
 HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPIC FACTOR, AND ACTS
 AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
 CC IT HAS NO DETECTABLE PROTEASE ACTIVITY.
 CC -I- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
 DISULFIDE BOND.
 CC -I- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRPSIN FAMILY. PLASMINOGEN SUBFAMILY.
 CC -----
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 the European Bioinformatics Institute. There are no restrictions on its
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; D90334; BAA14348.1; -;
 DR EMBL; D90318; BAA14348.1; JOINED.
 DR EMBL; D90319; BAA14348.1; JOINED.
 DR EMBL; D90320; BAA14348.1; JOINED.
 DR EMBL; D90322; BAA14348.1; JOINED.
 DR EMBL; D90323; BAA14348.1; JOINED.
 DR EMBL; D90324; BAA14348.1; JOINED.
 DR EMBL; D90325; BAA14348.1; JOINED.
 DR EMBL; D90326; BAA14348.1; JOINED.

DR EMBL: D90327: BAA14348.1: JOINED.
 DR EMBL: D90328: BAA14348.1: JOINED.
 DR EMBL: D90329: BAA14348.1: JOINED.
 DR EMBL: D90330: BAA14348.1: JOINED.
 DR EMBL: D90331: BAA14348.1: JOINED.
 DR EMBL: D90332: BAA14348.1: JOINED.
 DR EMBL: D90333: BAA14348.1: JOINED.
 DR EMBL: M29145: AAA52650.1: -
 DR EMBL: M60718: AAA52648.1: -
 DR EMBL: X16323: CAA34387.1: -
 DR EMBL: M73239: AAA64239.1: -
 DR EMBL: M73240: AAA64297.1: -
 DR EMBL: AC004960: AAC71655.1: -
 DR EMBL: M75983: AAG53460.1: -
 DR EMBL: M75972: AAG53460.1: JOINED.
 DR EMBL: M75973: AAG53460.1: JOINED.
 DR EMBL: M75974: AAG53460.1: JOINED.
 DR EMBL: M75975: AAG53460.1: JOINED.
 DR EMBL: M75976: AAG53460.1: JOINED.
 DR EMBL: M75977: AAG53460.1: JOINED.
 DR EMBL: M75978: AAG53460.1: JOINED.
 DR EMBL: M75979: AAG53460.1: JOINED.
 DR EMBL: M75980: AAG53460.1: JOINED.
 DR EMBL: M75981: AAG53460.1: JOINED.
 DR EMBL: M75982: AAG53460.1: JOINED.
 DR PIR: JH0579: JH0579.
 DR PIR: S06794: S06794.
 DR PDB: 2HGF: 24-JUN-98.
 DR PDB: 1BHT: 18-NOV-98.
 DR MEROPS: S01.976: -
 DR GlycoSuiteDB: P14210: -
 DR MIM: 142409: -
 DR InterPro: IPR001314: Chymotrypsin.
 DR InterPro: IPR000001: Kringle.
 DR InterPro: IPR003014: PAN.
 DR InterPro: IPR003609: Pan_app.
 DR InterPro: IPR001254: Trypsin.
 DR Pfam: PF00051: kringle_4.
 DR Pfam: PF00024: PAN: 1.
 DR Pfam: PF00089: trypsin_1.
 DR PRINTS: PR00722: CHYMOTRYPSIN.
 DR PRINTS: PR00018: KRINGLE.
 DR SMART: SM00130: KR: 4.
 DR SMART: SM00473: PAN_AP: 1.
 DR SMART: SM00020: TRYPSIN: 1.
 DR PROSITE: PS00021: TRYPSIN_DOM: 1.
 DR PROSITE: PS00070: KRINGLE_2: 4.
 DR PROSITE: PS00240: TRYPSIN_DOM: 1.
 DR Growth factor; Kringle; Glycoprotein; Serine protease homolog;
 KW Signal; 3D-structure.
 FT SIGNAL 1 31
 FT CHAIN 32 494 HEPATOCYTE GROWTH FACTOR ALPHA CHAIN.
 FT MOD_RES 495 728 HEPATOCYTE GROWTH FACTOR BETA CHAIN.
 FT MOD_RES 32 32 PYRROLIDONE CARBOXYLIC ACID.
 FT DOMAIN 127 127 PAP.
 FT DOMAIN 128 206 KRINGLE 1.
 FT DOMAIN 211 288 KRINGLE 2.
 FT DOMAIN 305 383 KRINGLE 3.
 FT DOMAIN 391 469 KRINGLE 4.
 FT DOMAIN 485 728 SERINE PROTEASE-LIKE.
 FT DISULFID 70 96
 FT DISULFID 74 84
 FT DISULFID 128 206
 FT DISULFID 149 189
 FT DISULFID 177 201
 FT DISULFID 487 604 INTERCHAIN (BY SIMILARITY).
 Query Match 69.3%; Score 52; DB 1; Length 728;
 Best Local Similarity 72.7%; Pred. No. 0.61;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 178 RNPGEBCGPW 188
 RESULT 15
 HGF_MOUSE
 ID HGF_MOUSE STANDARD: PRT: 728 AA.
 AC 008048; Q64007; Q61662;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hepatocyte growth factor precursor (Scatter factor) (SF)
 DE (Hepatopoietin A).
 GN HGF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 [1]
 RE SEQUENCE FROM N.A., AND SEQUENCE OF 496-504.
 RC TISSUE=Mammary fibroblast;
 RX MEDLINE=94183257; PubMed=8135822;
 RA Sasaki M., Nishio M., Sasaki T., Enami J.;
 RT "Identification of mouse mammary fibroblast-derived mammary growth
 factor as hepatocyte growth factor";
 RL Biochem. Biophys. Res. Commun. 199:772-779(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94363381; PubMed=8081873;
 RA Lee C.C., Kozak G.A., Yamada K.M.;
 RT "Structure, genetic mapping, and expression of the mouse Hgf/scatter
 factor gene";
 RL Cell Adhes. Commun. 1:101-111(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94060105; PubMed=8241272;
 RA Liu Y., Michalopoulos G.K., Zarnegar R.;
 RT "Molecular cloning and characterization of cDNA encoding mouse
 hepatocyte growth factor";
 RL Biochim. Biophys. Acta 1216:299-303(1993).
 CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
 HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPIC FACTOR, AND ACTS
 AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
 CC IT HAS NO DETECTABLE PROTEASE ACTIVITY.
 CC -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
 DISULFIDE BOND.
 CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM OF HGF IS PRODUCED BY
 ALTERNATIVE RNA SPLICING. THE SEQUENCE SHOWN HERE IS THAT OF THE
 LONG FORM.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D10212: BAA01064.1: -
 DR EMBL: D10213: BAA01065.1: -
 DR EMBL: S71816: AAB31855.1: -
 DR EMBL: X72307: CAA51054.1: ALT_INIT.
 DR HSSP: P14210: 1BHT.
 DR MGD: MGI:96079; Hgf.
 DR InterPro: IPR001314: Chymotrypsin.
 DR InterPro: IPR000001: Kringle.
 DR InterPro: IPR003014: PAN.
 DR InterPro: IPR003609: Pan_app.
 DR InterPro: IPR001254: Trypsin.

DR Pfam: PF00051; kringle; 4.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 4.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS00021; KRINGLE_1; 4.
 DR PROSITE: PS50070; KRINGLE_2; 4.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR Growth factor: Kringle; Glycoprotein; Serine protease homolog;
 KW Signal: Alternative splicing.
 FT SIGNAL 1 32
 FT CHAIN 33 495
 FT CHAIN 496 728
 FT MOD_RES 33 33
 FT
 FT DOMAIN 33 128
 FT DOMAIN 129 207
 FT DOMAIN 212 289
 FT DOMAIN 306 384
 FT DOMAIN 392 470
 FT DOMAIN 496 728
 FT DISULFID 71 97
 FT DISULFID 75 85
 FT DISULFID 488 607
 FT CARBOHYD 293 295
 FT CARBOHYD 403 403
 FT CARBOHYD 569 569
 FT CARBOHYD 656 656
 FT VARSPLIC 163 167
 FT CONFLICT 344 344
 FT CONFLICT 479 479
 FT CONFLICT 564 564
 SQ SEQUENCE 728 AA; 82944 MW; A0381FC497534328 CRC64;

Query Match 69.3%; Score 52; DB 1; Length 728;

Best Local Similarity 72.7%; Pred. No. 0.61; Mismatches 1; Indels 0; Gaps 0;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNPDDVGVGFW 11
 ||| | : |||
 Db 179 RNPGEVGVGFW 189

Search completed: November 8, 2002, 09:33:52
 Job time: 10.3333 secs

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PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PS
 XX
 PS Disclosure; Page 611; 733pp; English.
 CC
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 CC
 XX
 SQ Sequence 23 AA:
 Query Match 100.0%; Score 138; DB 22; Length 23;
 Best Local Similarity 100.0%; Pred. No. 4.4e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RNPDGVDGGMWATYTNPKRLDY 23
 Db 1 RNPDGVDGGMWATYTNPKRLDY 23
 AAB36570 standard; Peptide; 23 AA.
 XX
 AC AAB36570;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Mammalian kringle 5 peptide SEQ ID NO:9.
 XX
 XX Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory;
 KW vasotrophic; cytosolic; antirheumatic; antiproliferative; antidiabetic;
 KW antiarteriosclerotic; osteoparitic; angiogenesis inhibitor; angiogenesis;
 KW inflammatory disorder; inflammation; chronic articular rheumatism;
 KW psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis;
 KW capillary proliferation; atherosclerotic plaque; osteoporosis;
 KW cancer; solid tumour; angiofibroma; retrolental fibroplasia;
 KW haemangioma; Kasposi's sarcoma; neovascularisation; tumour growth.
 XX
 OS Homo sapiens.
 XX
 PN WO200070665-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-1B00763.
 XX
 PR 17-MAY-1999; 99US-0134406.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Rasamooliso M, Thibaudau K, Huang X, Belliveau R;
 XX
 DR WPI; 2001-090970/10.

XX
 PT New modified anti-angiogenic kringle 5 peptides capable of forming
 PT conjugates with blood proteins, useful for treating angiogenesis,
 PT inappropriate invasion of vessels or cancers in humans or mammals
 PS
 XX
 PS Claim 5; Page 9; 82pp; English.
 CC
 CC The present invention describes a modified anti-angiogenic peptide (I)
 CC comprising a reactive group that reacts with amino groups, hydroxyl
 CC groups or thiol groups on blood components to form stable covalent
 CC bonds. The reactive group is selected from succinimide or maleimido
 CC groups. (I) can have anti-inflammatory, vasotropic, cytosolic,
 CC antirheumatic, antiproliferative, antidiabetic, antiarteriosclerotic and
 CC osteoparitic activities, and is an angiogenesis inhibitor. (I) are useful
 CC for treating angiogenesis in a human, where the derivative is reacted
 CC with blood proteins. (I) are also useful for manufacturing a medicament
 CC extending the in vivo half-life of a kringle 5 peptide in a patient to
 CC provide an anti-angiogenic effect. In particular, a modified kringle 5
 CC peptide can be used for treating inflammatory disorders (e.g. immune and
 CC non-immune inflammation, chronic articular rheumatism or psoriasis),
 CC disorders associated with inappropriate or inappropriate invasion of
 CC vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis,
 CC capillary proliferation in atherosclerotic plaques or osteoporosis), or
 CC cancer associated disorders (e.g. solid tumours, solid tumour
 CC metastases, angiofibromas, retrolental fibroplasia, haemangiomas,
 CC Kasposi's sarcoma or other cancers requiring neovascularisation to
 CC support tumour growth). The peptides are useful for treating these
 CC diseases in mammalian or human patients. AAB36562 represents a mammalian
 CC kringle 5 protein, and AAB36563 to AAB36577 represent specifically
 CC claimed kringle 5 peptides from the present invention.
 CC
 XX
 SQ Sequence 23 AA:
 Query Match 100.0%; Score 138; DB 22; Length 23;
 Best Local Similarity 100.0%; Pred. No. 4.4e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RNPDGVDGGMWATYTNPKRLDY 23
 Db 1 RNPDGVDGGMWATYTNPKRLDY 23
 AAB92090 standard; Peptide; 24 AA.
 XX
 AC AAB92090;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Laminin fragment SEQ ID NO:1266.
 XX
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimide; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US13576.
 XX
 PR 17-MAY-1999; 99US-0134406.
 XX
 PR 10-SEP-1999; 99US-0134406.
 XX
 PR 15-OCT-1999; 99US-0139783.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 XX

DR WPI: 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
PS Disclosure: Page 609; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 24 AA:
Query Match 100.0%; Score 138; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 4,6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RNPDSVGGPMATTPRKLYD 23
DB 1 RNPDSVGGPMATTPRKLYD 23
RESULT 4
AAB92095
ID AAB92095 standard; Peptide: 24 AA.
XX
XX AAB92095;
AC
XX
XX 22-JUN-2001 (first entry)
DT
XX
XX Laminin fragment SEQ ID NO:1271.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
OS
XX
XX WO200069900-A2.
PN
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR
XX
XX 10-SEP-1999; 99US-0153406.
PR
XX
XX 15-OCT-1999; 99US-0159783.
PA
XX
XX (CONJ-) CONJUCHEM INC.
PI
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI
XX
XX WPI: 2001-112059/12.
DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT

XX
XX Disclosure; Page 611; 733pp; English.
PS
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 24 AA:
Query Match 100.0%; Score 138; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 4,6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RNPDSVGGPMATTPRKLYD 23
DB 1 RNPDSVGGPMATTPRKLYD 23
RESULT 5
AAB36565
ID AAB36565 standard; Peptide: 24 AA.
XX
XX AAB36565;
AC
XX
XX 09-MAR-2001 (first entry)
DT
XX
XX Mammalian kringle 5 peptide SEQ ID NO:4.
DE
XX
XX Kringle 5; anti-angiogenic; modified; blood protein; anti-inflammatory;
KW vasotropic; cytostatic; antirheumatic; antidiabetic;
KW antiarteriosclerotic; osteopathic; angiogenesis inhibitor; angiogenesis;
KW inflammatory disorder; inflammation; chronic articular rheumatism;
KW psoriasis; diabetic retinopathy; neovascular glaucoma; restenosis;
KW capillary proliferation; atherosclerotic plaque; osteoporosis;
KW cancer; solid tumour; angiodioma; retrorenal fibroplasia;
KW haemangioma; Kasposi's sarcoma; neovascularisation; tumour growth.
XX
XX
OS Mammalia.
OS
XX
XX WO200070665-A2.
PN
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-IB00763.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX
XX Bridon DP, Rasmoeliso M, Thibaudau K, Huang X, Belliveau R;
PI
XX
XX WPI: 2001-090970/10.
DR
XX
XX New modified anti-angiogenic kringle 5 peptides capable of forming
PT conjugates with blood proteins, useful for treating angiogenesis,
PT inappropriate invasion of vessels or cancers in humans or mammals
XX
XX Claim 5; Page 9; 82pp; English.
XX

CC The present invention describes a modified anti-angiogenic peptide (1)
 CC comprising a reactive group that reacts with amino groups, hydroxyl
 CC groups or thiol groups on blood components to form stable covalent
 CC bonds. The reactive group is selected from succinimidyl or maleimido
 CC groups. (1) can have anti-inflammatory, vasotropic, cytostatic,
 CC antithrombotic, antiproliferative, antidiabetic, antiarteriosclerotic and
 CC osteoprotective activities, and is an angiogenesis inhibitor. (1) are useful
 CC for treating angiogenesis in a human, where the derivative is reacted
 CC with blood proteins. (1) are also useful for manufacturing a medicament
 CC extending the in vivo half-life of a kringle 5 peptide in a patient to
 CC provide an anti-angiogenic effect. In particular, a modified kringle 5
 CC peptide can be used for treating inflammatory disorders (e.g. immune and
 CC non-immune inflammation, chronic articular rheumatism or psoriasis),
 CC disorders associated with inappropriate or inappropriate invasion of
 CC vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis,
 CC capillary proliferation in atherosclerotic plaques or osteoporosis), or
 CC cancer associated disorders (e.g. solid tumours, solid tumour
 CC metastases, angiodysplasias, retrolental fibroplasia, haemangiomas,
 CC Kaposi's sarcoma or other cancers requiring neovascularisation to
 CC support tumour growth). The peptides are useful for treating these
 CC diseases in mammalian or human patients. AAB36562 represents a mammalian
 CC kringle 5 protein, and AAB36563 to AAB36577 represent specifically
 CC claimed kringle 5 peptides from the present invention.

CC Sequence 24 AA;

Query Match 100.0%; Score 138; DB 22; Length 24;

Best Local Similarity 100.0%; Pred. No. 4.6e-11;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNPDDGVGPMAYTTNPKRLDY 23

Db 1 RNPDDGVGPMAYTTNPKRLDY 23

RESULT 6

AAM19256

ID AAM19256 standard; Peptide: 79 AA.

AC AAM19256;

DT 27-FEB-1998 (first entry)

DE Human plasminogen kringle 5 fragment.

KW Plasminogen; Kringle 5; cell proliferation inhibitor; angiogenesis;

KW diagnosis; therapeutic.

OS Homo sapiens.

XX W09723500-A1.

PD 03-JUL-1997.

PF 13-DEC-1996; 96WO-US20447.

PR 12-DEC-1996; 96US-0763528.

PR 13-DEC-1995; 95US-0008519.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Cao Y, Folkman MJ;

DR WPI; 1997-350965/32.

XX Plasminogen Kringle 5 peptide - which inhibits endothelial cell

PT proliferation, useful to treat angiogenesis mediated diseases and in

PT detection and diagnosis

XX Claim 1; Page 8; 51pp; English.

CC This sequence is an isolated fragment of the Kringle 5 peptide
 CC corresponding to amino acid 462 of the human plasminogen protein which

CC can be used in a novel method to inhibit endothelial cell proliferation
 CC activity. The protein can be used to treat angiogenesis mediated
 CC diseases, e.g. haemangioma, solid tumours, leukaemia, metastasis,
 CC telangiectasia, psoriasis, scleroderma, pyogenic granuloma, myocardial
 CC angiogenesis, plaque neovascularisation, coronary or cerebral
 CC collaterals, arteriovenous malformations, ischemic limb angiogenesis,
 CC corneal diseases, rubecosis, neovascular glaucoma, diabetic retinopathy,
 CC retrolental fibroplasia, arthritis, diabetic neovascularisation,
 CC muscular degeneration, peptic ulcer, Helicobacter related disease,
 CC fractures, keloids, vasculogenesis, haemotopiasis, ovulation,
 CC menstruation, placental or cat scratch fever, and to stimulate wound
 CC healing. The protein and antibodies generated from it can be used to
 CC screen for agonists and antagonists or in detection, imaging and
 CC diagnosis.

CC Sequence 79 AA;

Query Match 97.1%; Score 134; DB 18; Length 79;

Best Local Similarity 95.7%; Pred. No. 4.8e-10;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDDGVGPMAYTTNPKRLDY 23

Db 52 RNPDDGVGPMAYTTNPKRLDY 74

RESULT 7

AAB01914

ID AAB01914 standard; Protein; 90 AA.

AC AAB01914;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringle 5 (Val454-Ala543).

KW Plasminogen; human; kringle domain; endothelial cell proliferation;

KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;

KW antiproliferative; antiinflammatory; antitumor; antineurotic; antiarthritic;

KW antiangiogenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

XX US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

PR 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

PA (ABBO) ABBOTT LAB.

PI Davidson DJ;

DR WPI; 2000-349573/30.

XX Preparation of Kringle five peptide fragment for treating various

PT disorders such as angiogenic, ocular, skin diseases and cancer,

PT involves mixing mammalian plasminogen and elastase followed by

PT incubation and isolation -

PS Example 17; Page -; 48pp; English.

CC The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
 CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours

CC from the full length human plasminogen sequence (AAB01887) shown in
 CC figure 1.
 XX
 SQ Sequence 93 AA;
 Query Match 97.1%; Score 134; DB 21; Length 93;
 Best Local Similarity 95.7%; Pred. No. 5.7e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 RNPDDVGSPMAYTNPRLDY 23
 |||
 Db 60 RNPDDVGSPMAYTNPRLDY 82

RESULT 10
 AAB01913
 ID AAB01913 standard; Protein: 95 AA.
 XX
 AC AAB01913;
 XX
 DT 18-SEP-2000 (first entry)
 XX
 DE Human plasminogen kringle 5 (Val449-Ala543).
 XX
 KW Plasminogen; human; kringle domain; endothelial cell proliferation;
 KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
 KW angiotensin; antiinflammatory; antiulcer; antineumatic; antiarthritic;
 KW antiangiogenic; cancer; tumour; autoimmune disease.
 KW
 OS Homo sapiens.
 XX
 PN US6057122-A.
 XX
 PD 02-MAY-2000.
 XX
 PF 05-MAY-1997; 97US-0851350.
 XX
 PR 03-MAY-1996; 96US-0643219.
 PR 03-APR-1997; 97US-0832087.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Davidson DJ;
 XX
 DR WPI: 2000-349573/30.
 XX
 PT Preparation of Kringle five peptide fragment for treating various
 PT disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -
 XX
 PS Example 17; Page -: 48pp; English.
 XX
 CC The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
 CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukaemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber
 CC Syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01906-B01919 represent fragments of human plasminogen used
 CC in an exemplification of the invention.
 CC Note: This sequence is not shown in the specification, but is derived

CC from the full length human plasminogen sequence (AAB01887) shown in
 CC figure 1.
 XX
 SQ Sequence 95 AA;
 Query Match 97.1%; Score 134; DB 21; Length 95;
 Best Local Similarity 95.7%; Pred. No. 5.8e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 RNPDDVGSPMAYTNPRLDY 23
 |||
 Db 65 RNPDDVGSPMAYTNPRLDY 87

RESULT 11
 AAB01916
 ID AAB01916 standard; Protein: 98 AA.
 XX
 AC AAB01916;
 XX
 DT 18-SEP-2000 (first entry)
 XX
 DE Human plasminogen kringle 5 (Val449-Phe546).
 XX
 KW Plasminogen; human; kringle domain; endothelial cell proliferation;
 KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
 KW angiotensin; antiinflammatory; antiulcer; antineumatic; antiarthritic;
 KW antiangiogenic; cancer; tumour; autoimmune disease.
 KW
 OS Homo sapiens.
 XX
 PN US6057122-A.
 XX
 PD 02-MAY-2000.
 XX
 PF 05-MAY-1997; 97US-0851350.
 XX
 PR 03-MAY-1996; 96US-0643219.
 PR 03-APR-1997; 97US-0832087.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Davidson DJ;
 XX
 DR WPI: 2000-349573/30.
 XX
 PT Preparation of Kringle five peptide fragment for treating various
 PT disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -
 XX
 PS Example 17; Page -: 48pp; English.
 XX
 CC The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
 CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukaemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber
 CC Syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01906-B01919 represent fragments of human plasminogen used
 CC in an exemplification of the invention.
 CC Note: This sequence is not shown in the specification, but is derived

CC from the full length human plasminogen sequence (AAB01897) shown in
 CC figure 1.

XX Sequence 98 AA;

Query Match 97.1%; Score 134; DB 21; Length 98;
 Best Local Similarity 95.7%; Pred. No. 6e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNPDDGVGPMAYTTPRKLYDY 23
 |||||||||
 DB 65 RNPDDGVGPMCTTTPRKLYDY 87

RESULT 12

AAW34286
 ID AAW34286 standard; protein: 101 AA.

XX AAW34286;

DT 14-MAY-1998 (first entry)

XX Human kringle 5 peptide fragment.

XX Plasminogen; human; Kringle 5 peptide; anti-angiogenesis agent; cancer;
 KW metastatic solid tumour; carcinoma; lymphoma; haemangioma;
 KW psoriasis; arthritis; macular degeneration; diabetic retinopathy;
 KW autoimmune disease; ocular disease; capillary proliferation; therapy;
 KW kringle 5 receptor.

XX Homo sapiens.

PN WO9741824-A2.

PD 13-NOV-1997.

PF 05-MAY-1997; 97WO-US077700.

PR 03-APR-1997; 97US-0832087.

PR 03-APR-1996; 96US-0643219.

XX (ABBO) ABBOTT LAB.

PI Davidson DJ, Gubbins EJ, Wang J;

DR WPI; 1997-558670/51.

XX New kringle 5 peptide(s) and fusion proteins derived from
 PT plasminogen - useful as anti-angiogenesis agents for treating
 PT cancer, psoriasis, arthritis etc., including gene therapy

XX Claim 35; Fig 2; 78pp; English.

XX This sequence is a kringle 5 (K5) peptide homologous to human
 CC plasminogen. K5 peptide fragments homologous to this sequence, are
 CC anti-angiogenesis agents, specifically for treating or preventing cancer,
 CC particularly primary or metastatic solid tumours, carcinomas, sarcomas,
 CC lymphomas, haemangiomas. They can also be used for treating or preventing
 CC psoriasis, arthritis, macular degeneration and diabetic retinopathy. The
 CC fragments can also be used to treat autoimmune or ocular diseases,
 CC capillary proliferation within atherosclerotic plaque, haemophilic
 CC joints, wound granulation, ulcers etc., also as contraceptives that
 CC inhibit ovulation and establishment of the placenta. K5 antisera or
 CC (ant)agonists can be used similarly, optionally coupled to cytotoxic
 CC agents. Antagonists may be used to induce angiogenesis, e.g. for wound
 CC healing. The K5 peptides are also used to raise specific antibodies (Ab),
 CC for diagnosis and for affinity purification of K5 receptors. The K5
 CC receptors may then be expressed in tumour cells to increase their
 CC response to the peptides or used for identification of smaller
 CC antagonists. The Ab are used to detect/quantify the peptides in
 CC biological samples. The K5 peptides (and K5 fusion proteins) selectively
 CC inhibit proliferation of endothelial cells with low toxicity against
 CC normal cells. Typically they have 800-times greater inhibitory activity

CC against bovine capillary cells in vitro than kringle 1-4 peptides.

XX Sequence 101 AA;

Query Match 97.1%; Score 134; DB 18; Length 101;
 Best Local Similarity 95.7%; Pred. No. 6.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNPDDGVGPMAYTTPRKLYDY 23
 |||||||||
 DB 71 RNPDDGVGPMCTTTPRKLYDY 93

RESULT 13

AAB01890
 ID AAB01890 standard; Protein: 101 AA.

XX AAB01890;

DT 18-SEP-2000 (first entry)

XX Human plasminogen kringle 5, SEQ ID NO:34.

XX Plasminogen; kringle 5 domain; endothelial cell proliferation;
 KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
 KW antipsoriatic; antiinflammatory; antiulcer; antineumatic; antiarthritis;
 KW antilangiolitic; cancer; tumour; autoimmune disease.

XX Homo sapiens.

PN US6057122-A.

PD 02-MAY-2000.

PF 05-MAY-1997; 97US-0851350.

PR 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

XX (ABBO) ABBOTT LAB.

PI Davidson DJ;

DR WPI; 2000-349573/30.

XX Preparation of Kringle five peptide fragment for treating various
 PT disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -

XX Disclosure; Fig 2; 48pp; English.

XX The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300 followed by mammalian plasminogen and
 CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Weber
 CC Syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC disease and ulcers). The peptides are also useful as a birth control
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01890-B01894 represent, respectively, human, mouse, Rhesus
 CC monkey, bovine and porcine plasminogen kringle 5 domains.

XX Sequence 101 AA;

Query Match 97.1%; Score 134; DB 21; Length 101;
 Best Local Similarity 95.7%; Pred. No. 6.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDCVGGPMAYTTNPKRLYDY 23
 |||
 DB 71 RNPDCVGGPMCYTTNPKRLYDY 93

RESULT 14

AAB01912
 ID AAB01912 standard; Protein; 101 AA.

AC AAB01912;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringle 5 (Val443-Ala543).

KW Plasminogen; human; kringle domain; endothelial cell proliferation;
 KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
 KW antiposrotic; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
 KW antiangiogenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

PN US6057122-A.

PD 02-MAY-2000.

PE 05-MAY-1997; 97US-0851350.

PR 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

PA (ABBO) ABBOTT LAB.

PI Davidson DJ;

DR WPI; 2000-349573/30.

PT Preparation of Kringle five peptide fragment for treating various
 PT disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -

PS Example 17; Page -: 48pp; English.

CC The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
 CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukaemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
 CC syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01906-B01919 represent fragments of human plasminogen used
 CC in an exemplification of the invention.
 CC Note: This sequence is not shown in the specification, but is derived
 CC from the full length human plasminogen sequence (AAB01887) shown in
 CC figure 1.

XX Sequence 101 AA;

Query Match 97.1%; Score 134; DB 21; Length 101;
 Best Local Similarity 95.7%; Pred. No. 6.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDCVGGPMAYTTNPKRLYDY 23
 |||
 DB 71 RNPDCVGGPMCYTTNPKRLYDY 93

RESULT 15

AAB01915
 ID AAB01915 standard; Protein; 104 AA.

AC AAB01915;

DT 18-SEP-2000 (first entry)

DE Human plasminogen kringle 5 (Val443-Phe546).

KW Plasminogen; human; kringle domain; endothelial cell proliferation;
 KW angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic;
 KW antiposrotic; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
 KW antiangiogenic; cancer; tumour; autoimmune disease.

OS Homo sapiens.

PN US6057122-A.

PD 02-MAY-2000.

PE 05-MAY-1997; 97US-0851350.

PR 03-MAY-1996; 96US-0643219.

PR 03-APR-1997; 97US-0832087.

PA (ABBO) ABBOTT LAB.

PI Davidson DJ;

DR WPI; 2000-349573/30.

PT Preparation of Kringle five peptide fragment for treating various
 PT disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -

PS Example 17; Page -: 48pp; English.

CC The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
 CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful
 CC for treating angiogenic diseases, primary and metastatic solid tumours
 CC and carcinomas of various organs such as breast, genital tract,
 CC endocrine glands, skin, tumours of the brain and eyes and solid tumours
 CC arising from haematopoietic malignancies such as leukaemias and
 CC lymphomas. They are also used for the prophylaxis of various autoimmune
 CC diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases
 CC (e.g., psoriasis), blood vessel diseases (e.g. haemangiomas, Osler-Webber
 CC syndrome), diseases caused by excessive or abnormal stimulation of
 CC endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
 CC which have angiogenesis as a pathologic consequence (e.g., cat scratch
 CC agent which inhibits ovulation and establishment of the placenta.
 CC Sequences AAB01906-B01919 represent fragments of human plasminogen used
 CC in an exemplification of the invention.
 CC Note: This sequence is not shown in the specification, but is derived
 CC from the full length human plasminogen sequence (AAB01887) shown in
 CC figure 1.

XX Sequence 104 AA;

Query Match 97.1%; Score 134; DB 21; Length 192;
 Best Local Similarity 95.7%; Pred. No. 1.2e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPdGVGGPMAYTTNPKRLYDY 23
 |||||
 Db 159 RNPdGVGGPMAYTTNPKRLYDY 181

RESULT 18

AAU32126
 ID AAU32126 standard; Protein; 266 AA.

XX
 AC AAU32126;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #2617.

XX Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic

XX vaccination, testing and therapy -

XX Claim 20; Page 558; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The

XX polypeptides and antibodies to the polypeptides are useful for

XX determining the presence of or predisposition to a disease associated

XX with altered levels of polypeptide. The polypeptides are also useful for

XX identifying agents (agonists and antagonists) that bind to them. Cells

XX expressing the proteins are useful for identifying a therapeutic agent

XX for use in treatment of a pathology related to aberrant expression or

XX physiological interactions of the polypeptide. Vectors comprising

XX the nucleic acids encoding the polypeptides and cells genetically

XX engineered to express them are also useful for producing the proteins.

XX The proteins are useful in genetic vaccination, testing and

XX therapy, and can be used as nutritional supplements. They may be used to

XX increase stem cell proliferation; to regulate haematopoiesis; and in

XX bone, cartilage, tendon and/or nerve tissue growth or regeneration;

XX immune suppression and/or stimulation; as anti-inflammatory agents; and

XX in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid

XX sequences of novel human secreted proteins of the invention.

XX SQ Sequence 266 AA;

XX Query Match 97.1%; Score 134; DB 22; Length 266;

XX Best Local Similarity 95.7%; Pred. No. 1.6e-09;

XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX QY 1 RNPdGVGGPMAYTTNPKRLYDY 23

XX |||||

XX Db 109 RNPdGVGGPMAYTTNPKRLYDY 131

RESULT 19

AAU32129
 ID AAU32129 standard; Protein; 266 AA.

XX AAU32129;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #2620.

XX Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic

XX vaccination, testing and therapy -

XX Claim 20; Page 559; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The

XX polypeptides and antibodies to the polypeptides are useful for

XX determining the presence of or predisposition to a disease associated

XX with altered levels of polypeptide. The polypeptides are also useful for

XX identifying agents (agonists and antagonists) that bind to them. Cells

XX expressing the proteins are useful for identifying a therapeutic agent

XX for use in treatment of a pathology related to aberrant expression or

XX physiological interactions of the polypeptide. Vectors comprising

XX the nucleic acids encoding the polypeptides and cells genetically

XX engineered to express them are also useful for producing the proteins.

XX The proteins are useful in genetic vaccination, testing and

XX therapy, and can be used as nutritional supplements. They may be used to

XX increase stem cell proliferation; to regulate haematopoiesis; and in

XX bone, cartilage, tendon and/or nerve tissue growth or regeneration;

XX immune suppression and/or stimulation; as anti-inflammatory agents; and

XX in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid

XX sequences of novel human secreted proteins of the invention.

XX SQ Sequence 266 AA;

XX Query Match 97.1%; Score 134; DB 22; Length 266;

XX Best Local Similarity 95.7%; Pred. No. 1.6e-09;

XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX QY 1 RNPdGVGGPMAYTTNPKRLYDY 23

XX |||||

XX Db 109 RNPdGVGGPMAYTTNPKRLYDY 131

XX RESULT 20

XX AAU32136

XX ID AAU32136 standard; Protein; 266 AA.

XX AC AAU32136;

XX XX

DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #2627.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20; Page 561; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 266 AA;
 XX
 QY 1 RNPDDVGGPWAYTTNPKRLDY 23
 DB 109 RNPDDVGGPWCYTTNPKRLDY 131
 XX
 RESULT 21
 AAB08407
 ID AAB08407 standard; Protein: 271 AA.
 XX
 AC AAB08407;
 XX
 DT 20-DEC-2000 (first entry)
 XX
 DE A human angiogenesis inhibitor designated KED.
 XX
 KW Angiogenesis inhibitor; KED; kringie protein; angiogenesis; tPA;
 KW tissue plasminogen activator; tumour; atherosclerosis; arthritis;
 KW retinopathy; bronchial vascular congestion; inflammatory bowel disease;
 KW adult respiratory distress syndrome; Castleman's disease; psoriasis;
 KW

KW hepatitis; aneurysm; renal disease; haemangioma.
 XX
 OS Homo sapiens.
 XX
 PN WO200049871-A1.
 XX
 PD 31-AUG-2000.
 XX
 PF 24-FEB-2000; 2000WO-US04798.
 XX
 PR 24-FEB-1999; 99US-0121341.
 PR 25-FEB-1999; 99US-0121633.
 PR 18-NOV-1999; 99US-0166176.
 XX
 PA (FORD-) FORD HEALTH SYSTEM HENRY.
 XX
 PI Dou D, Chopp M, Wang L, Mikkelsen T;
 XX
 DR WPI; 2000-572016/53.
 DR N-PSDB; AAA64013.
 XX
 PT Use of kringie protein and kringie derived from plasminogen and
 PT composition comprising kringie proteins for treating tumor and
 PT atherosclerosis, arthritis and retinopathy -
 XX
 PS Disclosure; Page 151; 163pp; English.
 XX
 CC The present sequence represents a human polypeptide which is a potent
 CC angiogenesis inhibitor, designated KED. The KED polypeptide, kringie
 CC proteins, or a kringie derived from human tissue plasminogen activator
 CC (tPA) protein are used to inhibit angiogenesis. Kringie protein, KED
 CC or tPA are useful for treating tumours, as well as atherosclerosis,
 CC arthritis, retinopathy and other similar diseases. KED is also useful
 CC for the treatment of diseases such as bronchial vascular congestion,
 CC inflammatory bowel disease, adult respiratory distress syndrome,
 CC Castleman's disease, psoriasis, hepatitis, aneurysm, renal disease
 CC and haemangioma.
 XX
 SQ Sequence 271 AA;
 XX
 QY 1 RNPDDVGGPWAYTTNPKRLDY 23
 DB 56 RNPDDVGGPWCYTTNPKRLDY 78
 XX
 RESULT 22
 AAY25408
 ID AAY25408 standard; Protein: 357 AA.
 XX
 AC AAY25408;
 XX
 DT 08-SEP-1999 (first entry)
 XX
 DE Human tissue factor clone NuV129 protein.
 XX
 KW Tissue factor; human; thrombogenic; substructure; thrombose; tumour;
 KW vasculative malformation; vascular endothelium; NuV129.
 XX
 OS Homo sapiens.
 XX
 PN WO9932143-A1.
 XX
 PD 01-JUL-1999.
 XX
 PF 22-DEC-1998; 98WO-US27498.
 XX
 PR 23-DEC-1997; 97US-0996744.
 XX
 PA (NUVA-) NUVAS LLC.

XX Dickinson CD, Houston IL;
 XX
 PI WPI: 1999-405116/34.
 DR N-PSDB; AAX78893.
 XX
 PT New thrombogenic polypeptides used to, e.g. obliterate vasculature
 PT malformations
 XX
 PS Claim 30; Page 85-88; 97pp; English.
 XX
 CC This invention describes novel thrombogenic polypeptides which comprise a
 CC thrombogenic substructure and a context-dependent entity which recognizes
 CC desired biologically susceptible sites, e.g. tumour vascular endothelium.
 CC A novel context-dependent functional entity comprises a substructure with
 CC thrombogenic potential and one or more context-enhancing substructures
 CC having the ability to recognize desired biologically susceptible sites,
 CC where the entity imparts thrombogenic activity when positioned in the
 CC function-forming context at the biologically susceptible sites, and the
 CC entity has no thrombogenic activity absent a function-forming context at
 CC the biologically susceptible sites. The context-dependent functional
 CC entities impart thrombogenic activity only at biologically susceptible
 CC sites. They can be used to obliterate vasculature malformations or to
 CC selectively thrombose the vasculature of solid tumours. This sequence
 CC represents the human tissue factor protein NuV129 which is used in the
 CC method of the invention.
 CC
 SQ Sequence 357 AA;
 XX
 XX
 Query Match 97.1%; Score 134; DB 20; Length 357;
 Best Local Similarity 95.7%; Pred. No. 2.2e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RNPDGVDGPGWATYTNPRKLYDY 23
 Db 96 RNPDGVDGPGWCTYTNPRKLYDY 118
 XX
 RESULT 23
 AAR22502
 ID AAR22502 standard; Protein: 371 AA.
 XX
 AC AAR22502;
 XX
 DT 25-AUG-1992 (first entry)
 XX
 DE [GARSYQ]-[Plasminogen 443-541]-[t-PA 262-527] hybrid.
 XX
 KW Plasminogen; tissue plasminogen activator; hybrid; fibrinolysis;
 KW blood clotting; acute myocardial infarction.
 XX
 FH Key Location/Qualifiers
 FT Region 1..6
 FT Region /note= "amino acids -3 to +3 of t-PA"
 FT Region 7..105
 FT Region /note= "amino acids 443-541 of plasminogen"
 FT Region 106..371
 FT Region /note= "amino acids 262-527 of t-PA"
 FT Cleavage-site 119..120
 FT /note= "t-PA cleavage site"
 XX
 PN W09204450-A.
 XX
 PD 19-MAR-1992.
 XX
 PF 29-AUG-1991; 91WO-GB01455.
 XX
 PR 01-SEP-1990; 90GB-0019120.
 XX
 PA (BEEC) BEECHAM GROUP PLC.
 XX
 PI Dodd I, Brown M, Robinson JH;
 XX

DR WPI: 1992-114357/14.
 XX
 PT Hybrid plasminogen activators for treating thrombotic diseases -
 PT comprise Kringles 5 or Kringles 4 and 5 of plasminogen linked to
 PT B-chain of t-PA or u-PA via aminoacid sequence
 XX
 PS Claim 9; Page 50; 64pp; English.
 XX
 CC This hybrid plasminogen/t-PA sequence is described in the
 CC specification although the sequence itself is not given. The
 CC sequence given here has been compiled using the human plasminogen
 CC sequence from Patent No. W09013640 and the t-PA sequence of DE3930099.
 CC The variant 4-antisoYL [SYQ]-[Plasminogen 443-541]-[t-PA 262-527]
 CC is also specifically claimed. The hybrid fibrinolytic enzymes are
 CC useful in the treatment of thrombotic diseases.
 CC
 SQ See also AAR22499 and AAR22503-4.
 XX
 XX
 Query Match 97.1%; Score 134; DB 13; Length 371;
 Best Local Similarity 95.7%; Pred. No. 2.2e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RNPDGVDGPGWATYTNPRKLYDY 23
 Db 77 RNPDGVDGPGWCTYTNPRKLYDY 99
 XX
 RESULT 24
 AAR22504
 ID AAR22504 standard; Protein: 380 AA.
 XX
 AC AAR22504;
 XX
 DT 25-AUG-1992 (first entry)
 XX
 DE [GARSYQ]-[Plasminogen 443-541]-[u-PA 137-411] hybrid.
 XX
 KW Plasminogen; urokinase-like plasminogen activator; hybrid;
 KW fibrinolysis; blood clotting; acute myocardial infarction.
 XX
 FH Key Location/Qualifiers
 FT Region 1..6
 FT Region /note= "amino acids -3 to +3 of t-PA"
 FT Region 7..105
 FT Region /note= "amino acids 443-541 of plasminogen"
 FT Region 106..380
 FT Region /note= "amino acids 137-411 of u-PA"
 FT Cleavage-site 126..127
 FT /note= "u-PA cleavage site"
 XX
 PN W09204450-A.
 XX
 PD 19-MAR-1992.
 XX
 PF 29-AUG-1991; 91WO-GB01455.
 XX
 PR 01-SEP-1990; 90GB-0019120.
 XX
 PA (BEEC) BEECHAM GROUP PLC.
 XX
 PI Dodd I, Brown M, Robinson JH;
 XX
 DR WPI: 1992-114357/14.
 XX
 PT Hybrid plasminogen activators for treating thrombotic diseases -
 PT comprise Kringles 5 or Kringles 4 and 5 of plasminogen linked to
 PT B-chain of t-PA or u-PA via aminoacid sequence
 XX
 PS Claim 11; Page 50; 64pp; English.
 XX
 CC This hybrid plasminogen/u-PA sequence is described in the
 CC specification although the sequence itself is not given. The

CC sequence given here has been compiled using the human plasminogen
 CC sequence from Patent No. WO9013640 and the human u-PA sequence
 CC from the SWISSPROT database (UROK\$HUMAN). The hybrid fibrinolytic
 CC enzymes are useful in the treatment of thrombotic diseases.
 CC See also R22499, R22502 and R22503.

CC Sequence 380 AA;

Query Match 97.1%; Score 134; DB 13; Length 380;
 Best Local Similarity 95.7%; Pred. No. 2.3e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNPDDVGGMWYTTNPKRLDY 23
 |||||
 DB 77 RNPDDVGGMWYTTNPKRLDY 99

RESULT 25

AAW51457
 ID AAW51457 standard; protein; 437 AA.

XX AAW51457;

XX 02-SEP-1998 (first entry)

DE Human plasminogen fragment with neovascularisation inhibiting activity.

XX Human plasminogen; neovascularisation; angiotatin; inhibition;
 KW elastase; Sepharose.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 4..81
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 25..64
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 53..76
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 108..187
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 129..170
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 158..182
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 194..313
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 204..212
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 234..250
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 326..393
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 356..372
 FT Disulfide-bond /label= Disulphide_bond
 FT Disulfide-bond 383..411
 FT Disulfide-bond /label= Disulphide_bond

XX JP10158300-A.

XX 16-JUN-1998.

XX 28-NOV-1996; 96JP-0317250.

XX 28-NOV-1996; 96JP-0317250.

XX (SUZM) SUZUKI KK.

XX WPI; 1998-393476/34.

XX Human plasminogen derived polypeptide - has neovascularisation
 PT inhibiting activity
 XX

PS Claim 1; Page 2; 16pp: Japanese.

XX The invention relates to a neovascularisation inhibitor which comprises
 CC amino acids 355-791 of human plasminogen. Also claimed are a method for
 CC the preparation of angiotatin, and angiotatin prepared by this method.
 CC The human plasminogen protein fragment is prepared by: (a) applying human
 CC plasminogen to a lysine Sepharose column to separate it into plasminogen
 CC form 1 and form 2; (b) separating plasminogen form 1 and form 2 and
 CC digesting them with elastase; (c) fractionating the elastase-decomposed
 CC product of form 1 plasminogen and form 2 plasminogen to the lysine
 CC Sepharose column; (d) collecting the fractions bound to the lysine
 CC Sepharose column; (e) further fractionating the form 2 plasminogen using
 CC an Aminohexal Sepharose column; and (f) collecting the fraction bound to
 CC the Aminohexal Sepharose column. This human plasminogen fragment can be
 CC used to inhibit growth of vascular endothelial cells. The present
 CC sequence represents amino acids 355-791 of human plasminogen.

SQ Sequence 437 AA;

Query Match 97.1%; Score 134; DB 19; Length 437;
 Best Local Similarity 95.7%; Pred. No. 2.6e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNPDDVGGMWYTTNPKRLDY 23
 |||||
 DB 159 RNPDDVGGMWYTTNPKRLDY 181

RESULT 26

AAAR2499
 ID AAR2499 standard; protein; 467 AA.

XX AAR2499;

XX 25-AUG-1992 (first entry)

DE [GARSYO]-[Plasminogen 347-541]-[t-PA 262-527] hybrid.

XX Plasminogen; tissue plasminogen activator; hybrid; fibrinolysis;
 KW blood clotting; acute myocardial infarction.

XX Key Location/Qualifiers

FT Region 1..6
 FT Region /note= "amino acids -3 to +3 of t-PA"
 FT Region 7..201
 FT Region /note= "amino acids 347-541 of plasminogen"
 FT Region 202..467
 FT Region /note= "amino acids 262-527 of t-PA"
 FT Cleavage-site 215..216
 FT Cleavage-site /note= "t-PA cleavage site"

XX WO9204450-A.

XX 19-MAR-1992.

XX 29-AUG-1991; 91WO-GB01455.

XX 01-SEP-1990; 90GB-0019120.

XX (BEECH) BEECHAM GROUP PLC.

XX Dodd I, Brown M, Robinson JH;

XX WPI; 1992-114357/14.

XX Hybrid plasminogen activators for treating thrombotic diseases -
 PT comprise Kringles 5 or Kringles 4 and 5 of plasminogen linked to
 PT B-chain of t-PA or u-PA via aminoacid sequence

XX Claim 8; Page 50; 64pp: English.

XX This hybrid plasminogen/t-PA sequence is described in the
 CC specification although the sequence itself is not given. The

CC sequence given here has been compiled using the human plasminogen
 CC sequence from Patent No. WO9013640 and the t-PA sequence of DE3930099.
 CC A.N.N-Dimethyl-4-aminobenzoyl two-chain [SYO]-[plasminogen 347-541]-
 CC [t-PA 262-527] and the 4-anisoyl version of this variant are also
 CC specifically claimed. The hybrid fibrinolytic enzymes are useful in
 CC the treatment of thrombotic diseases. See also AAR2502-4.
 CC XX

Sequence 467 AA;

Query Match 97.1%; Score 134; DB 13; Length 467;
 Best Local Similarity 95.7%; Pred. No. 2.8e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDDGVGPMWYTTNPKRLDY 23
 DB 173 RNPDDGVGPMWYTTNPKRLDY 195

RESULT 27

AAR22503
 ID AAR22503 standard; Protein: 476 AA.

AC AAR22503;

DT 25-AUG-1992 (first entry)

DE [GARSYO]-[Plasminogen 347-541]-[u-PA 137-411] hybrid.

XX plasminogen; urokinase-like plasminogen activator; hybrid;
 XX fibrinolysis; blood clotting; acute myocardial infarction.

PH Key Location/Qualifiers

FT Region 1..6

FT /note= "amino acids -3 to +3 of t-PA"

FT Region 7..201

FT /note= "amino acids 347-541 of plasminogen"

FT Region 202..476

FT /note= "amino acids 137-411 of u-PA"

FT Cleavage-site 222..223

FT /note= "u-PA cleavage site"

PN WO9204450-A.

PD 19-MAR-1992.

PF 29-AUG-1991; 91WO-GB01455.

PR 01-SEP-1990; 90GB-0019120.

PA (BEEC) BEECHAM GROUP PLC.

PI Dodd I, Brown M, Robinson JH;

DR WPI; 1992-114357/14.

XX Hybrid plasminogen activators for treating thrombotic diseases -

PT comprise Kringles 5 or Kringles 4 and 5 of plasminogen linked to

PT B-chain of t-PA or u-PA via aminoacid sequence

PS Claim 10; Page 50; 64pp; English.

CC This hybrid plasminogen/u-PA sequence is described in the
 CC specification although the sequence itself is not given. The
 CC sequence given here has been compiled using the human plasminogen
 CC sequence from Patent No. WO9013640 and the human u-PA sequence
 CC from the SWISSPROT database (DROKSHUMAN). The hybrid fibrinolytic
 CC enzymes are useful in the treatment of thrombotic diseases.
 CC See also R22499, R22502 and R22504.
 CC XX

Sequence 476 AA;

Query Match 97.1%; Score 134; DB 13; Length 476;
 Best Local Similarity 95.7%; Pred. No. 2.9e-09;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDDGVGPMWYTTNPKRLDY 23
 DB 173 RNPDDGVGPMWYTTNPKRLDY 195

RESULT 28

AAV02100
 ID AAV02100 standard; Protein: 566 AA.

AC AAV02100;

DT 16-JUL-1999 (first entry)

DE A multifunctional protein of the invention.

XX Angiostatin; endostatin; interferon; thrombospondin;
 XX interferon-inducible protein; platelet factor 4; anti-angiogenic;
 XX anti-tumor; multifunctional protein; angiogenic-mediated disease;
 XX cancer; diabetic retinopathy; macular degeneration; arthritis;
 XX tumor cell production.

OS Synthetic.

XX Homo sapiens.

PN WO9916889-A1.

PD 08-APR-1999.

PF 30-SEP-1998; 98WO-US20464.

PR 01-OCT-1997; 97US-0060609.

PA (SEAR) SEARLE & CO G D.

PI Bolanowski MA, Caparon MH, Casperson GF, Gregory SA;

PI Klein BK, McKearn JP;

DR WPI; 1999-255098/21.

XX New multifunctional proteins useful for treating angiogenic-mediated

PT diseases

PS Claim 5; Page 95-96; 121pp; English.

CC The specification describes multifunctional proteins which comprise
 CC combinations of angiostatin, endostatin, interferon, thrombospondin,
 CC interferon-inducible protein and platelet factor 4, and have
 CC anti-angiogenic and/or anti-tumor activity. The multifunctional protein
 CC may exhibit useful properties such as having similar or greater
 CC biological activity when compared to a single factor or by having
 CC improved half-life or decreased adverse side effects, or a combination
 CC of these properties. The proteins can be used for treating an
 CC angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular
 CC degeneration, or arthritis. They can also be used for inhibiting the
 CC production of tumor cells (characteristic of lung, breast, ovarian,
 CC prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma,
 CC hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor
 CC growth. The present sequence represents a multifunctional protein of the
 CC invention.
 CC XX

Sequence 566 AA;

Query Match 97.1%; Score 134; DB 20; Length 566;
 Best Local Similarity 95.7%; Pred. No. 3.4e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDDGVGPMWYTTNPKRLDY 23
 DB 532 RNPDDGVGPMWYTTNPKRLDY 554

RESULT 29
 AAR60519
 ID AAR60519 standard; Protein: 790 AA.
 XX
 XX AAR60519;
 XX
 DT 22-MAR-1995 (first entry)
 XX
 DE Human 'Glu' plasminogen.
 XX
 KW Serine protease; Factor-Xa; recognition site; plasminogen; kringles;
 KW fusion protein cleavage; protein folding; primer;
 KW polymerase chain reaction; amplification.
 XX
 OS Homo sapiens.
 XX
 PN WO9418227-A.
 XX
 PD 18-AUG-1994.
 XX
 PF 04-FEB-1994; 94WO-DK00054.
 XX
 PR 04-FEB-1993; 93DK-0000130.
 PR 05-FEB-1993; 93DK-0000139.
 PR 03-DEC-1993; 93WO-GB02492.
 XX
 PA (DENZ-) DENZYME APS.
 XX
 PI Etzerodt M, Holtet TL, Thøgersen HC;
 XX
 DR WPI; 1994-279681/34.
 XX
 PT Refolding of polypeptide molecules - using a cyclic process
 PT involving denaturing and renaturing conditions to produce a
 PT correctly folded prod
 XX
 PS Disclosure; Page 148-50; 202pp; English.
 XX
 CC cDNA encoding kringles 1 and 4 of human plasminogen (full
 CC sequence given in AAR60519) was PCR amplified using primers given in
 CC AAO11268-71. Amplified cDNA was linked to a sequence encoding the
 CC Factor-Xa cleavage site (given in AAR60503), subcloned in vector
 CC pLICIMCH6 so that it was linked to a hexahistidine-encoding
 CC sequence and expressed in E. coli OY13. The fusion protein was
 CC purified on an Ni2+-activated NTA-agarose column. A cyclic
 CC procedure was used to obtain correctly folded recombinant protein.
 XX
 SQ Sequence 790 AA;
 XX
 Query Match 97.1%; Score 134; DB 15; Length 790;
 Best Local Similarity 95.7%; Pred. No. 4.8e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 RNPdGdVGPWATYTNPRKLYDY 23
 |||||||||
 DB 512 RNPdGdVGPWCYTTNPRKLYDY 534

KW capillary proliferation; atherosclerotic plaque; osteoporosis;
 KW cancer; solid tumour; angiofibroma; retrofental fibroplasia;
 KW haemangioma; Kasposi's sarcoma; neovascularisation; tumour growth.
 XX
 OS Mammalia.
 XX
 PN WO200070665-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000NO-IB00763.
 XX
 PR 17-MAY-1999; 99US-0134406.
 XX
 PA (CONJ-) CONJUNCHEM INC.
 XX
 PI Bridon DP, Rasameeliso M, Thibaudau K, Huang X, Bellevau R;
 XX
 DR WPI; 2001-090970/10.
 XX
 PT New modified anti-angiogenic kringles 5 peptides capable of forming
 PT conjugates with blood proteins, useful for treating angiogenesis,
 PT inappropriate invasion of vessels or cancers in humans or mammals
 XX
 PS Disclosure; Page 74-77; 82pp; English.
 XX
 CC The present invention describes a modified anti-angiogenic peptide (I)
 CC comprising a reactive group that reacts with amino groups, hydroxyl
 CC groups or thiol groups on blood components to form stable covalent
 CC bonds. The reactive group is selected from succinimidyl or maleimido
 CC groups. (I) can have anti-inflammatory, vasotropic, cyostatic,
 CC antirheumatic, antipsoriatic, antidiabetic, antarteriosclerotic and
 CC osteoplastic activities, and is an angiogenesis inhibitor. (I) are useful
 CC for treating angiogenesis in a human, where the derivative is reacted
 CC with blood proteins. (I) are also useful for manufacturing a medicament
 CC extending the in vivo half-life of a kringles 5 peptide in a patient to
 CC provide an anti-angiogenic effect. In particular, a modified kringles 5
 CC peptide can be used for treating inflammatory disorders (e.g. immune and
 CC non-immune inflammation, chronic articular rheumatism or psoriasis),
 CC disorders associated with inappropriate or inopportune invasion of
 CC vessels (e.g. diabetic retinopathy, neovascular glaucoma, restenosis,
 CC capillary proliferation in atherosclerotic plaques or osteoporosis), or
 CC cancer associated disorders (e.g. solid tumours, solid tumour
 CC metastases, angiofibromas, retrofental fibroplasia, haemangiomas,
 CC Kasposi's sarcoma or other cancers requiring neovascularisation to
 CC support tumour growth). The peptides are useful for treating these
 CC diseases in mammalian or human patients. AAB36562 represents a mammalian
 CC kringles 5 protein, and AAB36563 to AAB36577 represent specifically
 CC claimed kringles 5 peptides from the present invention.
 XX
 SQ Sequence 790 AA;
 XX
 Query Match 97.1%; Score 134; DB 22; Length 790;
 Best Local Similarity 95.7%; Pred. No. 4.8e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 RNPdGdVGPWATYTNPRKLYDY 23
 |||||||||
 DB 512 RNPdGdVGPWCYTTNPRKLYDY 534

RESULT 31
 AAB01887
 ID AAB01887 standard; Protein: 791 AA.
 XX
 XX AAB01887;
 XX
 DT 18-SEP-2000 (first entry)
 XX
 DE Human plasminogen, SEQ ID NO:1.
 XX
 KW Plasminogen; human; kringles 5 domain; endothelial cell proliferation;
 KW angiogenesis; antiproliferative; antarteriosclerotic; cyostatic;

KW antipsoriatic; antiinflammatory; antiulcer; antirheumatic; antiarthritic;
 KW antiangiogenic; cancer; tumour; autoimmune disease.
 OS Homo sapiens.
 XX
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 462..541
 FT Disulfide-bond 483..524
 FT Disulfide-bond 512..536
 FT Misc-difference 682
 FT /note= "Encoded by GTC"
 XX
 XX US6057122-A.
 XX
 XX PD 02-MAY-2000.
 XX
 XX PF 05-MAY-1997; 97US-0851350.
 XX
 XX PR 03-MAY-1996; 96US-0643219.
 PR 03-APR-1997; 97US-0832087.
 XX
 XX PA (ABBO) ABBOTT LAB.
 XX
 XX PI Davidson DJ;
 DR WPI: 2000-349573/30.
 DR N-PSDB: AAN52284.
 XX
 XX PT Preparation of Kringle five peptide fragment for treating various
 PT disorders such as angiogenic, ocular, skin diseases and cancer,
 PT involves mixing mammalian plasminogen and elastase followed by
 PT incubation and isolation -
 XX
 XX PS Example 17; Fig 1; 48pp; English.
 XX
 XX The invention relates to a method of preparing plasminogen kringle 5
 CC peptide fragments. The method comprises mixing mammalian plasminogen and
 CC elastase in the ratio 1:100-1:300, followed by incubating and isolating
 CC the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
 CC endothelial cell proliferation and migration. The peptides are useful for
 CC treating angiogenic diseases, primary and metastatic solid tumours and
 CC carcinomas of various organs such as breast, genital tract, endocrine
 CC glands, skin, tumours of the brain and eyes and solid tumours arising
 CC from haematopoietic malignancies such as leukaemias and lymphomas. They
 CC are also used for the prophylaxis of various autoimmune diseases (e.g.,
 CC rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis),
 CC blood vessel diseases (e.g. haemangiomas, Osler-Webber Syndrome),
 CC diseases caused by excessive or abnormal stimulation of endothelial cells
 CC (e.g., Crohn's disease, atherosclerosis), diseases which have
 CC angiogenesis as a pathologic consequence (e.g., cat scratch disease and
 CC ulcers). The peptides are also useful as a birth control agent which
 CC inhibits ovulation and establishment of the placenta. The present
 CC sequence represents human plasminogen.
 XX
 XX SQ Sequence 791 AA;
 XX
 XX Query Match 97.1%; Score 134; DB 21; Length 791;
 XX Best Local Similarity 95.7%; Pred. No. 4.8e-09;
 XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 1 RNPDDGVGPMAYTTNPKRLDY 23
 XX |||||
 XX Db 513 RNPDDGVGPMAYTTNPKRLDY 535

DE Human plasminogen.
 XX
 XX KW Human; serine protease zymogen; cardiant; thrombolytic;
 KW plasminogen activator; heart attack; stroke; blood clotting disorder.
 XX
 XX OS Homo sapiens.
 XX
 XX XX Key Location/Qualifiers
 FH Misc-difference 644..645
 FT Misc-difference 644..645
 FT /note= "specifically claimed in claim 6 of the
 FT specification"
 FT Misc-difference 542..791
 FT /note= "specifically claimed in claims 7 and 8 of the
 FT specification, preferably amino acids 562..791
 FT (claim 7)"
 XX
 XX PN WO200032759-A1.
 XX
 XX PD 08-JUN-2000.
 XX
 XX PF 06-MAY-1999; 99WO-US009991.
 XX
 XX PR 02-DEC-1998; 98US-0110588.
 XX
 XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 XX
 XX PI Lin X, Zhang XC, Tang JUN;
 DR WPI: 2000-422975/36.
 DR
 XX PT Polypeptide with plasminogen activator activity useful as thrombolytic
 PT agent for treating blood clot disorders e.g. heart attack, comprises 10
 PT amino acid peptide fragment for recognition or activation of
 PT plasminogen -
 XX
 XX PS Claim 6,7,8; Page 20-23; 41pp; English.
 XX
 XX The present sequence is plasminogen, the principal serine
 CC protease zymogen in the extracellular fluids of vertebrates. Its
 CC active form, plasmin, is implicated in pericellular proteolysis
 CC associated with a wide range of physiological and pathological
 CC processes. Plasminogen expression is regulated by plasminogen activators
 CC which hydrolyse a peptide bond in plasminogen to convert it to plasmin
 CC or form tight binding complexes with plasminogen to spontaneously
 CC convert it to plasmin. Review of sequence homologues of several
 CC plasminogen activators and chymotrypsin has identified a six amino acid
 CC peptide involved in plasminogen activation. This peptide is particularly
 CC useful when inserted between amino acid residues 644 and 645 of full
 CC length human plasminogen. Novel plasminogen activators have been made
 CC based upon the plasminogen activation/recognition site of plasminogen
 CC binding proteins. The polypeptides are useful in preparing thrombolytic
 CC agents for treating blood clotting disorders such as heart attack.
 XX
 XX SQ Sequence 791 AA;
 XX
 XX Query Match 97.1%; Score 134; DB 21; Length 791;
 XX Best Local Similarity 95.7%; Pred. No. 4.8e-09;
 XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 1 RNPDDGVGPMAYTTNPKRLDY 23
 XX |||||
 XX Db 513 RNPDDGVGPMAYTTNPKRLDY 535

RESULT 33
 AAY50867
 ID AAY50867 standard; protein; 791 AA.
 XX
 XX AC AAY50867;
 XX
 XX DT 24-FEB-2000 (first entry)
 XX
 XX Human plasminogen protein fragment.

XX Plasmalogen; human; thrombolytic agent; streptokinase; antigenic;
 KW blood clot; heart attack; treatment.
 XX
 OS Homo sapiens.
 XX WO9957251-A2.
 PN
 PD 11-NOV-1999.
 XX
 PF 06-MAY-1999; 99WO-US10086.
 XX
 PR 06-MAY-1998; 98US-0084392.
 XX
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 XX
 PI Zhang XC, Lin X, Tang JN;
 DR WPI; 2000-052966/04.
 XX
 PT New thrombolytic agents derived from modified humanized streptokinase,
 XX useful for treating blood clot disorders -
 PS Example 5; Page 40-43; 55pp; English.
 XX
 CC This invention describes a novel thrombolytic agent comprising
 CC streptokinase where at least one nonessential portion has been modified.
 CC The invention also describes a method of forming a thrombolytic agent
 CC comprising determining a nonessential portion of streptokinase and
 CC modifying the nonessential portion to render the resulting protein less
 CC antigenic. The modified streptokinase is used to treat blood clot
 CC disorders, such as heart attacks. The modified streptokinase has less
 CC antigenicity than streptokinase but is still able to complex plasminogen
 CC and lead to plasminogen activation. Modified streptokinase with the
 CC nonessential portions removed or truncated simplify the molecule. Such
 CC smaller proteins are cheaper and easier to produce. This sequence
 CC represents a fragment of the human plasminogen protein which is used in
 CC the description of the method of the invention.
 XX
 SQ Sequence 791 AA;
 QY
 Query Match 97.1%; Score 134; DB 21; Length 791;
 Best Local Similarity 95.7%; Pred. No. 4.8e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 RNPDDVGGPMWYTTNPKRLDY 23
 513 RNPDDVGGPMWYTTNPKRLDY 535
 RESULT 34
 AAG67223 standard; Protein: 791 AA.
 ID AAG67223;
 AC AAG67223;
 XX
 DT 13-NOV-2001 (first entry)
 XX
 DE Amino acid sequence of human plasminogen.
 XX
 KW Angiotatin; plasminogen; sulfydryl donor; angiogenesis; tumour;
 KW angiotatin; plasminogen; sulfydryl donor; angiogenesis; tumour;
 KW rheumatoid arthritis; atherosclerosis; ocular angiogenic disease;
 KW diabetic retinopathy; corneal graft rejection; cardiovascular disease;
 KW cerebral vascular disease; diabetes; immune disorder;
 KW chronic inflammation; autoimmunity.
 XX
 OS Homo sapiens.
 XX WO200158921-A2.
 PN
 PD 16-AUG-2001.

PF 08-FEB-2001; 2001WO-US04021.
 XX
 PR 08-FEB-2000; 2000US-0500397.
 XX
 PA (NOUN) UNIV NORTHWESTERN.
 XX
 PI Soff G, Gately ST, Twardowski P;
 DR WPI; 2001-550019/61.
 XX
 PF Producing angiotatin for treating angiogenic diseases involves
 PT contacting plasminogen with plasminogen activator and sulphydryl donor
 PT simultaneously, or producing plasmin which is contacted with sulphydryl
 PT donor -
 XX
 PS Disclosure; Page 77-80; 101pp; English.
 XX
 CC The specification describes a method for generating angiotatin in
 CC vitro. The method comprises contacting plasminogen with a sulphydryl
 CC donor, or culturing cells capable of producing plasminogen activator
 CC in conditioned culture medium (CCM) and contacting the CCM with
 CC plasminogen. Angiotatin produced by method of the invention is useful
 CC for treating animals with angiogenesis diseases. It is useful for
 CC treating an angiogenic disease such as neoplastic diseases (e.g. tumours
 CC and tumour metastasis), benign tumours (e.g. hemangiomas, acoustic
 CC neuromas, etc), connective tissue disorders (e.g. rheumatoid arthritis
 CC and atherosclerosis), ocular angiogenic diseases (e.g. diabetic
 CC retinopathy, corneal graft rejection, etc), cardiovascular diseases,
 CC cerebral vascular diseases, diabetes-associated diseases and immune
 CC disorders (e.g. chronic inflammation and autoimmunity). The present
 CC sequence represents a plasminogen.
 XX
 SQ Sequence 791 AA;
 QY
 Query Match 97.1%; Score 134; DB 22; Length 791;
 Best Local Similarity 95.7%; Pred. No. 4.8e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 RNPDDVGGPMWYTTNPKRLDY 23
 513 RNPDDVGGPMWYTTNPKRLDY 535
 RESULT 35
 AAR20013 standard; Protein: 807 AA.
 ID AAR20013;
 AC AAR20013;
 XX
 DT 31-MAR-1992 (first entry)
 XX
 DE PA mutant Plg 1-541 [Arg298-299->Gln298-299] t-PA 262-527.
 XX
 KW Fibrinolytic; plasminogen activator; Kringle; t-PA; thrombosis;
 KW myocardial infarction; cleavage site.
 XX
 XX
 FH Key Location/Qualifiers
 FH 1..541
 FT Region /label= "plasminogen
 FT /note= "residues 1-541, including Kringle
 FT Region 542..807
 FT /label= "t-PA
 FT /note= "[Arg298->Gln, Arg299->Gln]t-PA 262-527"
 XX
 PN WO9118989-A.
 XX
 PD 12-DEC-1991.
 XX
 PF 21-MAY-1991; 91WO-GB00801.
 XX
 PR 26-MAY-1990; 90GB-0011861.
 XX

XX	Castellino FU, whiteflect JL, Rosen ED, McLinden JH;
PI	
XX	WPI; 1990-361475/48.
DR	N-PSDB; AAQ06648.
XX	
PT	Expression of human plasminogen in eukaryotic cell vector - used
XX	in thrombolytic therapy
PS	Disclosure; Fig 2; 110pp; English.
XX	
CC	Plasminogen can be produced by culturing a eukaryotic cell lacking
CC	a site-specific plasminogen activator and comprising the DNA
CC	encoding this amino acid sequence.
CC	Pharmaceutical compns. containing plasminogen can be used for
CC	thrombolytic therapy.
XX	
SQ	Sequence 810 AA;
Query Match	97.1%; Score 134; DB 11; Length 810;
Best Local Similarity	95.7%; Pred. No. 4.9e-09;
Matches 22; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 RNPDCVYGCPWATTNPKRLVDY 23
Db	532 RNPDDGVGGPWCYTNPRLKYD 554
RESULT 37	
AA13219	
ID	AA13219 standard; Protein; 810 AA.
XX	
AC	AA13219;
XX	
DT	05-SEP-1991 (first entry)
XX	
DE	R561G human plasminogen variant.
XX	
KW	Plasminogen; proteolytic cleavage; variant; thrombosis; HPg.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	1..19
FT	/label= sig_peptide
FT	20..810
FT	/label= mat_protein
FT	103..182
FT	/label= kringle_1
FT	185..263
FT	/label= kringle_2
FT	273..353
FT	/label= kringle_3
FT	377..455
FT	/label= kringle_4
FT	481..561
FT	/label= kringle_5
FT	561..810
FT	/label= protein_protease
XX	
PN	WO9108297-A.
XX	
PD	13-JUN-1991.
XX	
PF	31-OCT-1990; 90WO-US06345.
XX	
PR	01-DEC-1989; 89US-0444584.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Castellino FU, Higgins D L;
XX	
DR	WPI; 1991-193201/26.

DR N-PSDB; AA011998.
XX
PT New human plasminogen variant with replaced ARG-561 - is
PT complexed with fibrinolytic enzyme for use in thrombolytic
PT therapy
PS
XX Disclosure; Fig 1(A-P); 82pp; English.
XX
CC The amino acid at position 475 is Val for the vector pUC119PN127.6,
CC whereas Fig 1 of the specification reflecting the sequence
CC encoding native human plasminogen, contains Ala. The amino acid at
CC 561 of the wild-type plasminogen (Arg), is substituted by any amino
CC acid except Lys. Here the amino acids is substituted by Gly.
CC Position 561 is the critical cleavage site in the conversion of
CC plasminogen to plasmin. The resulting product is proteolytic
CC resistant plasminogen which may be used to treat thrombosis in
CC humans. When complexed with streptokinase, it does not degrade into
CC plasmin and it caused rapid plasminogen activator activity.
XX
SQ Sequence 810 AA:
Query Match 97.1%; Score 134; DB 12; Length 810;
Best Local Similarity 95.7%; Pred. No. 4.9e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RNPDDVGGPMATYTNPKRLDY 23
Db 532 RNPDDVGGPMATYTNPKRLDY 554
|||||
RESULT 38
AAR12406
ID AAR12406 standard; Protein; 810 AA.
XX
AC AAR12406;
XX
DT 05-SEP-1991 (first entry)
XX
DE R561S human plasminogen variant.
XX
KW Plasminogen; proteolytic cleavage; variant; thrombosis; HPg.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Peptide 1..19
FT /label= sig_peptide
FT 20..810
FT Protein /label= mat_protein
FT 103..182
FT Domain /label= kringle_1
FT 185..263
FT Domain /label= kringle_2
FT 275..353
FT Domain /label= kringle_3
FT 377..455
FT Domain /label= kringle_4
FT 481..561
FT Domain /label= kringle_5
FT 561..810
FT Region /label= protein_protease
XX
FN W09108297-A.
XX
PD 13-JUN-1991.
XX
PF 31-OCT-1990; 90WO-US06345.
XX
PR 01-DEC-1989; 89US-0444584.
XX
PA (GETH) GENENTECH INC.
XX
PI Castellino FT, Higgins D L;

XX
DR WPT; 1991-193201/26.
XX
PT N-PSDB; AA011998.
XX
PT New human plasminogen variant with replaced ARG-561 - is
PT complexed with fibrinolytic enzyme for use in thrombolytic
PT therapy
PS
XX Disclosure; Fig 1(A-P); 82pp; English.
XX
CC The amino acid at position 475 is Val for the vector pUC119PN127.6,
CC whereas Fig 1 of the specification reflecting the sequence
CC encoding native human plasminogen, contains Ala. The amino acid at
CC 561 of the wild-type plasminogen (Arg), is substituted by any amino
CC acid except Lys. Here the amino acids is substituted by Glu.
CC Position 561 is the critical cleavage site in the conversion of
CC plasminogen to plasmin. The resulting product is proteolytic
CC resistant plasminogen which may be used to treat thrombosis in
CC humans. When complexed with streptokinase, it does not degrade into
CC plasmin and it caused rapid plasminogen activator activity.
XX
SQ Sequence 810 AA:
Query Match 97.1%; Score 134; DB 12; Length 810;
Best Local Similarity 95.7%; Pred. No. 4.9e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RNPDDVGGPMATYTNPKRLDY 23
Db 532 RNPDDVGGPMATYTNPKRLDY 554
|||||
RESULT 39
AAR13220
ID AAR13220 standard; Protein; 810 AA.
XX
AC AAR13220;
XX
DT 05-SEP-1991 (first entry)
XX
DE R561S human plasminogen variant.
XX
KW Plasminogen; proteolytic cleavage; variant; thrombosis; HPg.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Peptide 1..19
FT /label= sig_peptide
FT 20..810
FT Protein /label= mat_protein
FT 103..182
FT Domain /label= kringle_1
FT 185..263
FT Domain /label= kringle_2
FT 275..353
FT Domain /label= kringle_3
FT 377..455
FT Domain /label= kringle_4
FT 481..561
FT Domain /label= kringle_5
FT 561..810
FT Region /label= protein_protease
XX
FN W09108297-A.
XX
PD 13-JUN-1991.
XX
PF 31-OCT-1990; 90WO-US06345.
XX
PR 01-DEC-1989; 89US-0444584.
XX
PA (GETH) GENENTECH INC.

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XX  Castellino FJ, Higgins D L;
XX  WPI: 1991-193201/26.
XX  N-PSDB: AAQ11998.
XX
XX  New human plasminogen variant with replaced ARG-561 - is
XX  complexed with fibrinolytic enzyme for use in thrombolytic
XX  therapy
XX
XX  Disclosure: Fig 1(A-P); 82pp; English.
XX
XX  The amino acid at position 475 is Val for the vector pUC119PN127.6,
XX  whereas Fig 1 of the specification reflecting the sequence
XX  encoding native human plasminogen, contains Ala. The amino acid at
XX  561 of the wild-type plasminogen (Arg), is substituted by any amino
XX  acid except Lys. Here the amino acids is substituted by Ser.
XX  Position 561 is the critical cleavage site in the conversion of
XX  plasminogen to plasmin. The resulting product is proteolytic
XX  resistant plasminogen which may be used to treat thrombosis in
XX  humans. When complexed with streptokinase, it does not degrade into
XX  plasmin and it caused rapid plasminogen activator activity.
XX
XX  Sequence 810 AA;
XX
XX  Query Match 97.1%; Score 134; DB 12; Length 810;
XX  Best Local Similarity 95.7%; Pred. No. 4.9e-09;
XX  Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  1 RNPdGdVGGPMAYTTNPRKLYD 23
XX  |||||
XX  Db 532 RNPdGdVGGPMCYTTPRKLXYD 554

RESULT 40
AAR13221
ID AAR13221 standard; Protein; 810 AA.
XX
XX  AAR13221;
XX
XX  05-SEP-1991 (first entry)
XX
XX  Human plasminogen variant.
XX
XX  Plasminogen; proteolytic cleavage; variant; thrombosis; HPg.
XX
XX  Homo sapiens.
XX
XX  Key Location/Qualifiers
XX  Peptide 1..19 /label= sig_peptide
XX  Protein 20..810 /label= mat_protein
XX  Domain 103..182 /label= kringle_1
XX  Domain 185..263 /label= kringle_2
XX  Domain 275..353 /label= kringle_3
XX  Domain 377..455 /label= kringle_4
XX  Domain 481..561 /label= kringle_5
XX  Region 561..810 /label= protein_protease
XX
XX  WO9108297-A.
XX  13-JUN-1991.
XX
XX  31-OCT-1990; 90WO-US06345.
XX
XX  01-DEC-1989; 89US-0444584.

```

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XX  (GETH ) GENENTECH INC.
XX  Castellino FJ, Higgins D L;
XX  WPI: 1991-193201/26.
XX  N-PSDB: AAQ11998.
XX
XX  New human plasminogen variant with replaced ARG-561 - is
XX  complexed with fibrinolytic enzyme for use in thrombolytic
XX  therapy
XX
XX  Disclosure: Fig 1(A-P); 82pp; English.
XX
XX  The amino acid at position 475 is Val for the vector pUC119PN127.6,
XX  whereas Fig 1 of the specification reflecting the sequence
XX  encoding native human plasminogen, contains Ala. The amino acid at
XX  561 of the wild-type plasminogen (Arg), is substituted by any amino
XX  acid except Lys.
XX  Position 561 is the critical cleavage site in the conversion of
XX  plasminogen to plasmin. The resulting product is proteolytic
XX  resistant plasminogen which may be used to treat thrombosis in
XX  humans. When complexed with streptokinase, it does not degrade into
XX  plasmin and it caused rapid plasminogen activator activity.
XX
XX  Sequence 810 AA;
XX
XX  Query Match 97.1%; Score 134; DB 12; Length 810;
XX  Best Local Similarity 95.7%; Pred. No. 4.9e-09;
XX  Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  1 RNPdGdVGGPMAYTTNPRKLYD 23
XX  |||||
XX  Db 532 RNPdGdVGGPMCYTTPRKLXYD 554

RESULT 41
AAR12938
ID AAR12938 standard; Protein; 810 AA.
XX
XX  AAR12938;
XX
XX  23-SEP-1991 (first entry)
XX
XX  Plasminogen mutein T1 with thrombin cleavage site.
XX
XX  protease; fibrinolysis; blood clotting; thrombosis.
XX
XX  Key Location/Qualifiers
XX  Cleavage-site 578..580 /label= Thrombin cleavage site
XX
XX  WO9109118-A.
XX  27-JUN-1991.
XX
XX  07-DEC-1990; 90WO-G001912.
XX
XX  07-DEC-1989; 89GB-0027722.
XX  07-DEC-1990; 90WO-GB01911.
XX
XX  (BRIT-) BRIT BIO-TECHN LTD.
XX
XX  Dawson KM, Edwards RM, Forman JM;
XX
XX  WPI: 1991-208145/28.
XX  N-PSDB: AAQ12547.
XX
XX  Activatable fibrinolytic and antithrombotic proteins - activated by
XX  e.g. factor Xa, thrombin or activated protein C
XX
XX  Claim 7; Fig 2 and Fig 5; 73pp; English.

```

CC This protein is a plasminogen mutant cleavable by thrombin.
 CC Activation is localised to the thrombus because cleavage to plasmin
 CC is by an enzyme of the blood clotting pathway. Compositions
 CC comprising the mutant plasminogen are used for treatment or
 CC prevention of thrombosis, etc.
 CC See AAQ12542-Q12558.

XX Sequence 810 AA;

Query Match 97.1%; Score 134; DB 12; Length 810;
 Best Local Similarity 95.7%; Pred. No. 4.9e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNPDDGVGGPMAYTNPRLKLYD 23
 DB 532 RNPDDGVGGPMCTTNPRLKLYD 554

RESULT 42

AAAR34428

ID AAR34428 standard; Protein; 810 AA.

XX AAR34428;

DE 17-AUG-1993 (first entry)

XX Sequence encoded by a plasminogen cDNA.

KW Zymogen; fibrinolytic activity; cleavage.

OS Synthetic.

PN US5200340-A.

PD 06-APR-1993.

PF 22-MAY-1987; 87US-0053412.

PR 22-MAY-1987; 87US-0053412.

PA (ZYMO) ZYMOGENETICS INC.

PI Foster DC, Mulvihill ER, Ohara PJ, Pingel K, Yoshitake S;

DR MPI: 1993-133739/16.

DR N-PSDB; AAQ40319.

PT Human tissue plasminogen activator single chain form fibrinolytic

PT agent - comprises thrombin cleavable zymogen stimulating amido

PT lytic activity, for lysing clots in heart attack and stroke

XX victims and suppressing fibrin matrix

PS Example; Fig 10A, 10B, 10C; 22pp; English.

CC A lambda phage clone comprising a cDNA sequence encoding

CC plasminogen was obtained from Dr. Mark Marten at the University of

CC Washington. The cDNA was isolated from a human liver library by

CC probing with the partial sequence of Malinowski et al. The sequence

CC of the complete cDNA and the encoded amino acid sequence are shown

CC in AAQ40319 and AAR34428.

SQ Sequence 810 AA;

Query Match 97.1%; Score 134; DB 14; Length 810;
 Best Local Similarity 95.7%; Pred. No. 4.9e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNPDDGVGGPMAYTNPRLKLYD 23

DB 532 RNPDDGVGGPMCTTNPRLKLYD 554

RESULT 43

AAW31169

XX AAW31169 standard; Protein; 810 AA.

AC AAW31169;

DE 26-FEB-1998 (first entry)

XX Plasminogen protein for production of recombinant plasminogen.

KW Plasminogen; alpha-1-antitrypsin; AAT; argserpins; recombinant;

XX stabilising protein.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 60 /note= "encoded by ACC"

FT Misc-difference 191 /note= "encoded by GAA"

FT Misc-difference 223 /note= "encoded by AAA"

FT Misc-difference 280 /note= "encoded by GCT"

FT Misc-difference 291 /note= "encoded by CTG"

FT Misc-difference 395 /note= "encoded by GSA"

FT Misc-difference 503 /note= "encoded by CAG"

FT Misc-difference 607 /note= "encoded by TCT"

FT Misc-difference 615 /note= "encoded by CAG"

FT Misc-difference 658 /note= "encoded by TTG"

FT Misc-difference 709 /note= "encoded by GCT"

XX US5648254-A.

XX 15-JUL-1997.

XX 14-JUL-1994; 94US-0275076.

XX 04-DEC-1989; 89US-0445302.

XX 15-JAN-1988; 88US-0144357.

XX 28-OCT-1991; 91US-0785865.

XX 14-JUL-1994; 94US-0275076.

PA (ZYMO) ZYMOGENETICS INC.

PI Kumar AA, Mulvihill ER;

DR MPI: 1997-372063/34.

DR N-PSDB; AAT89686.

PT Production of recombinant plasminogen - by co-expression with

PT plasminogen-processing or -stabilising protein

XX Example 2; Fig 6A-D; 32pp; English.

PS This is the protein plasminogen. The encoding cDNA is used in a new

CC process for the production of plasminogen where a first DNA sequence

CC encoding plasminogen and at least one additional DNA sequence encoding a

CC protein that processes or stabilises the plasminogen is introduced into

CC a eukaryotic host cell. The protein is selected from alpha-1-antitrypsin

CC (AAT) and its variants and Argserpins. Both the DNA sequences are

CC operably linked to transcriptional promoter and terminator sequences. The

CC host cell is cultured under conditions that allow the DNA sequences to be

CC expressed and the recombinant plasminogen is isolated from the host cell.

CC Co-expression of plasminogen and the protein gives increased yields of

CC undegraded plasminogen.

SQ Sequence 810 AA:

Query Match 97.1%; Score 134; DB 18; Length 810;

Best Local Similarity 95.7%; Pred. No. 4.9e-09;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDDVGSPWATYTNPKRLYDY 23

Db 532 RNPDDVGSPWCTYTNPKRLYDY 554

RESULT 44

AAV08685

ID AAY08685 standard; Protein; 810 AA.

XX AAY08685;

DT 10-AUG-1999 (first entry)

XX Human plasminogen protein.

XX Plasminogen: human; angiotatin; endostatin; gene therapy; vector;

KW anti-angiogenic; attenuation; cytostatic; anti-diabetic; ophthalmology;

KW tumour growth; solid tumour; diabetic retinopathy; retina.

XX Homo sapiens.

XX WO926480-A1.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-US24950.

XX 20-NOV-1997; 97US-0975424.

XX (GENE-) GENETIX PHARM INC.

XX (MAST) MASSACHUSETTS INST. TECHNOLOGY.

XX Bachelot F, Leboulch P, Pawluc RJ;

XX WPI: 1999-357696/30.

XX N-PSDB: AAY77711.

XX Anti-angiogenic gene therapy vectors

XX Disclosure: Fig 5; 83pp; English.

This invention describes a novel viral gene therapy vector comprising a nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine angiotatin, human or murine endostatin and angiotenesis-inhibiting fusions and fragments, where the viral vector is sufficiently attenuated for use in human gene therapy. The products of the invention have anti-angiogenic, cytostatic, anti-diabetic and ophthalmological activity. The vector is used in gene therapy for inhibiting tumour growth in humans harbouring a solid tumour. The vector expresses an anti-angiogenic polypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis in the vicinity of the retina. The vector is administered to cells ex vivo and then administered to the patient.

SQ Sequence 810 AA:

Query Match 97.1%; Score 134; DB 20; Length 810;

Best Local Similarity 95.7%; Pred. No. 4.9e-09;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDDVGSPWATYTNPKRLYDY 23

Db 532 RNPDDVGSPWCTYTNPKRLYDY 554

RESULT 45

AAV02114

ID AAY02114 standard; Protein; 810 AA.

XX AAY02114;

DT 16-JUL-1999 (first entry)

DE SEQ ID 77 of WO9916889.

XX Angiotatin; endostatin; interferon; thrombospondin;

KW interferon-inducible protein; platelet factor 4; anti-angiogenic;

KW anti-tumor; multifunctional protein; angiogenic-mediated disease;

KW cancer; diabetic retinopathy; macular degeneration; arthritis;

KW tumor cell production.

XX Homo sapiens.

XX WO9916889-A1.

XX 08-APR-1999.

XX 30-SEP-1998; 98WO-US20464.

XX 01-OCT-1997; 97US-0060609.

XX (SEAR) SEARLE & CO G D.

XX Bolanowski MA, Caparon MH, Casperson GF, Gregory SA;

XX Klein BK, McKearn JP;

XX WPI: 1999-255098/21.

XX New multifunctional proteins useful for treating angiogenic-mediated diseases

XX Disclosure: Page 107-109; 121pp; English.

The specification describes multifunctional proteins which comprise combinations of angiotatin, endostatin, interferon, thrombospondin, CC interferon-inducible protein and platelet factor 4, and have CC anti-angiogenic and/or anti-tumor activity. The multifunctional protein CC may exhibit useful properties such as having similar or greater CC biological activity when compared to a single factor or by having CC improved half-life or decreased adverse side effects, or a combination CC of these properties. The proteins can be used for treating an CC angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular CC degeneration, or arthritis. They can also be used for inhibiting the CC production of tumor cells (characteristic of lung, breast, ovarian, CC prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, CC hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor CC growth. The present sequence is used in the course of the invention.

SQ Sequence 810 AA:

Query Match 97.1%; Score 134; DB 20; Length 810;

Best Local Similarity 95.7%; Pred. No. 4.9e-09;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDDVGSPWATYTNPKRLYDY 23

Db 532 RNPDDVGSPWCTYTNPKRLYDY 554

RESULT 46

AAV82690

ID AAY82690 standard; Protein; 810 AA.

XX AAY82690;

XX 09-AUG-2000 (first entry)

XX Human plasminogen angiotatin converting enzyme of pH4 (PACF4).

XX Human; cathepsin D precursor; PACF4; cancer; metastasis; inhibition;

KW		plasmaogen angiotatin converting enzyme of pH4; cytostatic;
KV		antidiabetic; ophthalmological; antirheumatic; solid tumour;
KW		diabetic retinopathy; rheumatism.
XX		
OS	Homo sapiens.	
PN	WO200020570-A1.	
XX		
PX	13-APR-2000.	
XX		
PF	29-SEP-1999; 99WO-JP05322.	
XX		
PR	02-OCT-1998; 98JP-0296095.	
PA	(KAGA) CHEMO-SERO-THERAPEUTIC RES INST.	
PI	Morikawa W, Kaminaka K, Takemoto S, Maeda H, Nozaki C, Miyamoto S;	
DR	WPI; 2000-303762/26.	
PT	Enzyme useful for treatment and prevention of tumor metastasis and	
PP	other diseases involving angiogenesis, splits plasma proteins to give	
PS	fragments capable of inhibiting cancer metastasis	
XX		
CC	Disclosure; Fig 7; 55pp; Japanese.	
CC	The present invention describes an enzyme (I) which splits plasma	
CC	proteins to give fragments which are capable of inhibiting cancer	
CC	metastasis. (I) has cytostatic, antidiabetic, ophthalmological and	
CC	antirheumatic activities. (I) splits plasma proteins to produce	
CC	fragments which can inhibit metastasis. (I) is useful for the	
CC	treatment and prevention of diseases in which angiogenesis plays a	
CC	part including solid tumours, diabetic retinopathy, and rheumatism.	
CC	The present sequence represents human plasminogen angiotatin converting	
CC	enzyme of pH4 (PACE4), which is used in the exemplification of the	
CC	present invention.	
SQ	Sequence 810 AA;	
QY	Query Match 97.1%; Score 134; DB 21; Length 810;	
	Best Local Similarity 95.7%; Pred. No. 4.9e-09;	
	Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
DB	1 RNPDGVGGPMAYTTNPKRLDY 23	
	532 RNPDGVGGPMCYTTPRKLYD 554	
RESULT 47		
ID	AAV53867 standard; protein; 810 AA.	
AC	AAV53867;	
DT	13-MAR-2000 (first entry)	
DE	Amino acid sequence of human plasminogen protein.	
KW	Human; plasminogen; angiotatin; greenstatin; thrombolytic factor;	
KV	angiogenesis inhibitory protein; proliferation; angiogenesis; cancer;	
KW	vascular endothelial cell; ophthalmic disease; glaucoma;	
KX	diabetic retinopathy; arthritis; psoriasis.	
OS	Homo sapiens.	
PN	WO9961464-A1.	
PD	02-DEC-1999.	
PF	28-MAY-1999; 99WO-KR00263.	
PR	28-MAY-1998; 98KR-0019535.	
PR	27-MAY-1999; 99KR-0019144.	

	PX	(GREC) KOREA GREEN CROSS CORP.
	XX	
	PI	You WK, So SH, Ahn BC, Lee H, Jung S, Kim Y, Lee JH, Hong Y;
	PI	Joe YA, Chang S;
	DR	WPI; 2000-086703/07.
	PT	Purifying angiogenesis inhibitors produced as recombinant proteins in
	PT	Escherichia coli, useful as anticancer agents and for treating ocular
	PT	diseases -
	PS	Disclosure; Page 41-45; 55pp; English.
	XX	
	CC	The present sequence represents the human plasminogen protein. Fragments
	CC	of the plasminogen protein, specifically angiotatin (comprising amino
	CC	acids 99-467) and greenstatin (comprising amino acids 101-354) are used
	CC	as thrombolytic factors and angiogenesis inhibitory proteins. Angiotatin
	CC	contains the kringle 1-4 region of plasminogen, and greenstatin contains
	CC	the kringle 1-3 region of plasminogen. As both proteins contain a high
	CC	number of disulphide bonds, they are difficult to purify. The
	CC	specification describes a method for the purification of such
	CC	angiogenesis inhibitory proteins. The method comprises solubilising
	CC	the proteins, produced as inclusion bodies in Escherichia coli and
	CC	retolding the solubilised fraction in buffer containing urea and
	CC	glutathione. The angiogenesis inhibitory proteins specifically inhibit
	CC	proliferation of vascular endothelial cells, but not that of
	CC	non-endothelial cancer or normal cells. The angiogenesis inhibitory
	CC	proteins are used to suppress angiogenesis, specifically for treating
	CC	cancers (e.g. of lung, skin and brain) or ophthalmic diseases (e.g.
	CC	glaucoma and diabetic retinopathy), but also arthritis and psoriasis.
	XX	
	SQ	Sequence 810 AA:
	Query Match	97.1%; Score 134; DB 21; Length 810;
	Best Local Similarity	95.7%; Pred. No. 4.9e-09;
	Matches 22; Conservative	0; Mismatches 1; Indels 0; Gaps 0,
OY	1 RNPDDGVGGPMAYTTPRKLYDY 23	
DB	532 RNPDGDVGGPMCYTNPRKLYDY 554	
RESULT 48		
AAR12933		
ID	AAR12933 standard; Protein; 811 AA.	
XX		
AC	AAR12933;	
DT	23-SEP-1991 (first entry)	
XX		
DZ		
DE	Plasminogen mutetin X1 with factor Xa cleavage site.	
XX		
KW	protease; fibrinolysis; blood clotting; thrombosis.	
XX		
FH	Key location/Qualifiers	
FT	Cleavage-site 578..581	
FT	/Label= Factor Xa cleavage site	
XX		
FN	WO9109118-A.	
PD	27-JUN-1991.	
XX		
FF	07-DEC-1990; 90WO-GO01912.	
XX		
PR	07-DEC-1989; 89GB-0027722.	
PR	07-DEC-1990; 90WO-CB01911.	
PA	(BRBI-) BRIT BIO-TECHN LTD.	
XX		
PI	Dawson KM, Edwards RM, Forman JM;	
OR	WPI; 1991-208145/28.	

DR N-PSDB; AAQ12542.
 XX
 PT Activatable fibrinolytic and antithrombotic proteins - activated by
 PT e.g. factor Xa, thrombin or activated protein C
 XX
 PS Claim 7; Fig 2 and Fig 4; 73pp; English.
 XX
 CC This protein is a plasminogen mutant cleavable by Factor Xa.
 CC Activation is localised to the thrombus because cleavage to plasmin
 CC is by an enzyme of the blood clotting pathway. Compositions
 CC comprising the mutant plasminogen are used for treatment or
 CC prevention of thrombosis, etc.
 CC See AAQ12543-Q12558.
 CC
 XX
 SQ Sequence 811 AA;
 Query Match 97.1%; Score 134; DB 12; Length 811;
 Best Local Similarity 95.7%; Pred. No. 4.9e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RNPDDVGSPWATYTNPKRLDY 23
 DB 532 RNPDDVGSPWCTYTNPKRLDY 554
 RESULT 49
 ID AAR12939 standard; Protein; 811 AA.
 AC AAR12939;
 XX
 DT 23-SEP-1991 (first entry)
 XX
 DE Plasminogen muterin T2 with thrombin cleavage site.
 KW protease; fibrinolysis; blood clotting; thrombosis.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 578..581
 FT /label= Thrombin cleavage site
 FT
 PN WO9109118-A.
 XX
 PD 27-JUN-1991.
 XX
 PF 07-DEC-1990; 90WO-GB01912.
 XX
 PR 07-DEC-1989; 89GB-0027722.
 PR 07-DEC-1990; 90WO-GB01911.
 XX
 PA (BRBI-) BRIT BIO-TECHN LTD.
 XX
 PI Dawson KM, Edwards RM, Forman JM;
 XX
 DR WPI; 1991-208145/28.
 DR N-PSDB; AAQ12548.
 XX
 PT Activatable fibrinolytic and antithrombotic proteins - activated by
 PT e.g. factor Xa, thrombin or activated protein C
 XX
 PS Claim 7; Fig 2 and Fig 5; 73pp; English.
 XX
 CC This protein is a plasminogen mutant cleavable by thrombin.
 CC Activation is localised to the thrombus because cleavage to plasmin
 CC is by an enzyme of the blood clotting pathway. Compositions
 CC comprising the mutant plasminogen are used for treatment or
 CC prevention of thrombosis, etc.
 CC See AAQ12542-Q12558.
 CC
 XX
 SQ Sequence 811 AA;
 Query Match 97.1%; Score 134; DB 12; Length 811;
 Best Local Similarity 95.7%; Pred. No. 4.9e-09;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RNPDDVGSPWATYTNPKRLDY 23
 DB 532 RNPDDVGSPWCTYTNPKRLDY 554
 RESULT 50
 ID AAR12943 standard; Protein; 811 AA.
 AC AAR12943;
 XX
 DT 23-SEP-1991 (first entry)
 XX
 DE Plasminogen muterin T13 with thrombin cleavage site.
 KW protease; fibrinolysis; blood clotting; thrombosis.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 579..583
 FT /note="recognised by thrombin"
 FT
 PN WO9109118-A.
 XX
 PD 27-JUN-1991.
 XX
 PF 07-DEC-1990; 90WO-GB01912.
 XX
 PR 07-DEC-1989; 89GB-0027722.
 PR 07-DEC-1990; 90WO-GB01911.
 XX
 PA (BRBI-) BRIT BIO-TECHN LTD.
 XX
 PI Dawson KM, Edwards RM, Forman JM;
 XX
 DR WPI; 1991-208145/28.
 DR N-PSDB; AAQ12552.
 XX
 PT Activatable fibrinolytic and antithrombotic proteins - activated by
 PT e.g. factor Xa, thrombin or activated protein C
 XX
 PS Claim 9; Fig 2 and Fig 5; 73pp; English.
 XX
 CC This protein is a plasminogen mutant cleavable by thrombin.
 CC Activation is localised to the thrombus because cleavage to plasmin
 CC is by an enzyme of the blood clotting pathway. Compositions
 CC comprising the mutant plasminogen are used for treatment or
 CC prevention of thrombosis, etc.
 CC See AAQ12542-Q12558.
 CC
 XX
 SQ Sequence 811 AA;
 Query Match 97.1%; Score 134; DB 12; Length 811;
 Best Local Similarity 95.7%; Pred. No. 4.9e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RNPDDVGSPWATYTNPKRLDY 23
 DB 532 RNPDDVGSPWCTYTNPKRLDY 554
 Search completed: November 8, 2002, 09:33:00
 Job time : 33 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:31:20 ; Search time 15 Seconds

(Without alignments)
147.337 Million cell updates/sec

Title: US-09-657-431-9

Perfect score: 138

Sequence: 1 RNPBGVGVGPWAYTTPRKLVDY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : PIR-71.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	97.1	810	1 PLHU	plasmin (EC 3.4.21
2	130	94.2	810	2 B30848	plasmin (EC 3.4.21
3	128	92.8	812	1 PLMS	plasmin (EC 3.4.21
4	124	89.9	460	2 B61345	plasmin (EC 3.4.21
5	120	87.0	810	2 I46260	plasmin (EC 3.4.21
6	117	84.8	4548	1 S00657	apoptotectin(a) (EC
7	114	82.6	455	2 A61545	plasmin (EC 3.4.21
8	113	81.9	790	1 PLPG	plasmin (EC 3.4.21
9	111	80.4	812	1 PLBO	plasmin (EC 3.4.21
10	94	68.1	716	1 JCS061	macrophage-stimula
11	92	66.7	711	1 A47136	macrophage-stimula
12	90	65.2	716	1 A40332	macrophage-stimula
13	82	59.4	728	1 A35644	hepatocyte growth
14	81	58.7	728	1 JH0579	hepatocyte growth
15	80	58.0	728	1 A60185	hepatocyte growth
16	80	58.0	625	1 TBBO	thrombin (EC 3.4.2
17	78	56.5	710	1 I51283	hepatocyte growth
18	75	55.8	169	2 A40522	plasmin (EC 3.4.21
19	75	54.3	411	2 I51285	hepatocyte growth
20	73	52.9	336	2 S33879	plasmin precursor
21	73	52.9	617	2 SI0511	thrombin (EC 3.4.2
22	72.5	52.5	2869	2 T18518	apolipoprotein(a)
23	71	51.4	618	2 A35827	thrombin (EC 3.4.2
24	71	51.4	622	1 TBHU	thrombin (EC 3.4.2
25	68.5	49.6	123	2 C61545	plasmin (EC 3.4.21
26	66.5	48.2	89	2 A60140	plasmin (EC 3.4.21
27	65.5	47.5	1420	2 A32869	apolipoprotein(a)
28	62.5	45.3	120	2 E61545	plasmin (EC 3.4.21
29	60	43.5	435	2 E70711	hypothetical prote

30	59	42.8	943	2 B45082	neurotrophic recep
31	56	40.6	559	1 A35029	t-plasminogen acti
32	56	40.6	559	1 A35029	t-plasminogen acti
33	53.5	38.8	153	2 T33719	probable lipoprote
34	52	37.7	323	2 T25094	hypothetical prote
35	52	37.7	562	1 UKHUT	t-plasminogen acti
36	51	37.0	194	2 T10851	y4h0 protein - Rhl
37	51	37.0	552	2 S36786	carboxylesterase (
38	51	37.0	564	1 S36787	t-plasminogen acti
39	50.5	36.6	394	2 JS0600	polyamine transpor
40	49	35.5	297	2 E83194	probable csp prote
41	49	35.5	539	2 G70520	coagulation factor
42	49	35.5	615	1 KFH012	ror-related recept
43	49	35.5	946	1 A47299	plasma membrane H+
44	48.5	35.1	961	2 T49228	hypothetical prote
45	48	34.8	268	2 B64318	hypothetical prote
46	48	34.8	347	2 T32768	hypothetical prote
47	48	34.8	357	2 T32881	2-oxoisovalerate d
48	48	34.8	410	2 AC3603	probable PLC prot
49	48	34.8	508	2 F70662	cell wall-binding
50	47	34.1	461	2 H84099	

ALIGNMENTS

RESULT 1

PLHU

Plasmin (EC 3.4.21.7) precursor [validated] - human

N:Alternate names: plasminogen precursor [misnomer]

N:Contains: angiotatin; microplasmin; plasmogen

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence-revision 02-Dec-1994 #text-change 15-Sep-2000

R:Peterson, T.E.; Martzen, W.R.; Ichinose, A.; Davie, E.W.

J. Biol. Chem. 265, 6104-6111, 1990

A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the f

A:Reference number: A35229; M01D:90202879

A:Accession: A35229

A:Molecule type: DNA

A:Residues: 1-810 <PEP>

A:Cross-references: GB:J05286; GB:M4276; M1D:9190064; P1D:AAA60113.1; P1D:9387026

A:Experimental source: leukocyte; lung fibroblast

R:Malgaroli, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.;

Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990

A:Title: Definition of the transcription initiation site of human plasminogen gene in

A:Reference number: I52242; M01D:91097523

A:Accession: I52242

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-16 <MALI>

A:Cross-references: GB:M62890; M1D:9190092; P1D:AAA6454.1; P1D:9553613

R:Forstner, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.

FEBS Lett. 213, 254-260, 1987

A:Title: Molecular cloning and characterization of a full-length cDNA clone for human

A:Reference number: A26646; M01D:87162490

A:Accession: A26646

A:Molecule type: mRNA

A:Residues: 1-471, 'D', 'A', '73-810 <FOR>

A:Cross-references: GB:X05199; M1D:935530; P1D:CAA28831.1; P1D:935531

A:Experimental source: liver

R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.

Biochemistry 23, 4243-4250, 1984

A:Title: Characterization of a complementary deoxyribonucleic acid coding for human a

A:Reference number: I45961; M01D:85023311

A:Accession: I62738

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 292-471, 'D', 'A', '73-810 <MAL2>

A:Cross-references: GB:K02922; M1D:9190112; P1D:AAA60124.1; P1D:9387031

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

- A:Residues: 367-419 <MAL3>
A:Cross-References: GB:K02921; NID:9190110; PIDN:AAA60123.1; PID:9190111
R:Brustholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,
A:Reference number: S03735; MUID:81212097
A:Accession: S03735
A:Molecule type: protein
A:Residues: 20-71, 'E', '73-76 <BRD>
R:Soltup-Jensen, L.; Petersen, T.E.; Magnusson, S.
submitted to the Atlas, July 1977
A:Reference number: A00929
A:Accession: A00929
A:Molecule type: protein
A:Residues: 20-71, 'E', '73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>
R:Wiman, B.
Eur. J. Biochem. 76, 129-137, 1977
A:Title: Primary structure of the B-chain of human plasmin.
A:Reference number: A04627; MUID:77225245
A:Accession: A04627
A:Molecule type: protein
A:Residues: 581-810 <WII>
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen
A:Reference number: A04625; MUID:75093329
A:Accession: A04625
A:Molecule type: protein
A:Residues: 20-50, 'Q', '51-71, 'E', '73-85, 87-100 <W12>
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen the
A:Reference number: A04626; MUID:76043692
A:Accession: A04626
A:Molecule type: protein
A:Residues: 483-507, 'E', 509-604 <W13>
R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summariia, L.
J. Biol. Chem. 248, 1631-1633, 1973
A:Title: The primary structure of human plasminogen. II. The histidine loop of human plasminogen
A:Reference number: A92125; MUID:73149248
A:Accession: A92125
A:Contents: annotation; active site
R:Groskopf, W.R.; Summariia, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
A:Reference number: A92048; MUID:69234739
A:Accession: A92048
A:Contents: annotation; active site
R:Trexler, M.; Valli, Z.; Pathy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A:Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
A:Reference number: A92382; MUID:82213905
A:Accession: A92382
A:Contents: annotation; omega-aminocarboxylic acid binding sites
R:Valli, Z.; Pathy, L.
J. Biol. Chem. 259, 13690-13694, 1984
A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
A:Reference number: A92458; MUID:85054794
A:Accession: A92458
A:Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
R:Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.;
J. Biol. Chem. 271, 29461-29467, 1996
A:Title: Kringle domains of human angiotensin. Characterization of the anti-proliferative
A:Reference number: A58811; MUID:97067211
A:Accession: A58811
A:Contents: annotation
R:Liljen, H.R.; Uguw, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A:Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (K
A:Reference number: A58812; MUID:9548733
A:Accession: A58812
A:Contents: annotation
R:Tullinsky, A.; Mulichak, A.M.
submitted to the Brookhaven Protein Data Bank, July 1991
A:Reference number: A51341; PDB:1PK4
A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
R:Tullinsky, A.; Wu, T.P.
submitted to the Brookhaven Protein Data Bank, July 1991
- A:Reference number: A51488; PDB:2PK4
A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
R:Wu, T.P.; Tullinsky, A.
submitted to the Brookhaven Protein Data Bank, August 1993
A:Reference number: A51911; PDB:1PKR
A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
R:Padmanabhan, K.; Tullinsky, A.
submitted to the Brookhaven Protein Data Bank, April 1994
A:Reference number: A52408; PDB:1PMK
A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
R:Tullinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A65244; PDB:1CEA
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R:Tullinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A65245; PDB:1CEB
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R:Mulichak, A.M.; Tullinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A:Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.
A:Reference number: A58819; MUID:92031502
A:Accession: A58819
A:Contents: annotation
R:Wu, T.P.; Padmanabhan, K.; Tullinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A:Title: The refined structure of the epsilon-aminocaproic acid complex of human plasminogen
A:Reference number: A58818; MUID:92031503
A:Accession: A58818
A:Contents: annotation
R:de Vos, A.M.; Ulsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tullinsky, A.; Westbrook, B.
Biochemistry 31, 270-279, 1992
A:Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at
A:Reference number: A39483; MUID:92118803
A:Accession: A39483
A:Contents: annotation; X-ray crystallography, 2.4 angstroms
R:Steck, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
submitted to the Brookhaven Protein Data Bank, June 1995
A:Reference number: A65980; PDB:1KRN
A:Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65803; PDB:1HPJ
A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A:Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
A:Reference number: S43645; MUID:94237157
A:Accession: S43645
A:Contents: annotation; conformation by (1)H-NMR, residues 96-184
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen
A:Reference number: A58817; MUID:94237158
A:Accession: A58817
A:Contents: annotation; conformation by (1)H-NMR
A:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many
A:Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKH
d PIR:FEHDB).
A:Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:THRA2) immediately
A:Comment: resulting in two chains connected by two disulfide bonds. Without the inhibi
A:Comment: Micropasmin is formed by autolytic cleavage of plasmin under artificial c
A:Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiotensin.
A:Comment: Solid tumors.
A:Gene: GDB:PLG
A:Cross-References: GDB:119498; OMIM:173350
A:Map position: 6q26-6q27
A:Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1;
A:Function:
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a
A:Description: the walls of the graafian follicle; also activates the urokinase-type plasminogen
A:Pathway: fibrinolysis
A:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol

C:Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd

F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-810/Product: plasminogen #status experimental <PRO>

F:20-96/Domain: activation peptide #status experimental <APT>

F:79-466/Product: angiotensin #status experimental <AST>

F:97-580,581-810/Product: plasmin #status experimental <MAT>

F:97-580/Domain: plasmin chain A #status experimental <CHA>

F:103-181/Domain: kringle homology <KR1>

F:185-262/Domain: kringle homology <KR2>

F:275-352/Domain: kringle homology <KR3>

F:377-454/Domain: kringle homology <KR4>

F:481-560/Domain: kringle homology <KR5>

F:550-580,581-810/Product: microplasmin #status experimental <MMT>

Query Match 97.1%; Score 134; DB 1; Length 810;
Best Local Similarity 95.7%; Pred. No. 1,6e-11;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDDVGGMATYTNPKRLDY 23
|||||
Db 532 RNPDDVGGMATYTNPKRLDY 554

RESULT 2

plasmin (EC 3.4.21.7) precursor - rhesus macaque

C:Species: Macaca mulatta (Rhesus macaque)

C:Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text_change 22-Jun-1999

C:Accession: B32869; B30848

R:Tomlinson, J. E.; McLean, J. W.; Lawn, R. M.
J. Biol. Chem. 264, 5957-5965, 1989

A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A:Reference number: A32869; MUID:89174660

A:Accession: B32869

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-810 <TOM>

A:Cross-references: GB:J04697; NID:q342272; PIDN:AAA36901.1; PID:q342273

C:Superfamily: Plasmin; Kringle homology; plasminogen-related protein precursor homology

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F:1-19/Domain: signal sequence #status predicted <SIG>

F:103-181/Domain: kringle homology <KR1>

F:185-262/Domain: kringle homology <KR2>

F:275-352/Domain: kringle homology <KR3>

F:377-454/Domain: kringle homology <KR4>

F:481-560/Domain: kringle homology <KR5>

F:581-803/Domain: trypsin homology <TRY>

F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
bonds: #status predicted

F:622,665,760/Active site: His, Asp, Ser #status predicted

Query Match 94.2%; Score 130; DB 2; Length 810;
Best Local Similarity 91.3%; Pred. No. 6.3e-11;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNPDDVGGMATYTNPKRLDY 23
|||||
Db 532 RNPDDVGGMATYTNPKRLDY 554

RESULT 3

plasmin (EC 3.4.21.7) precursor - mouse

N:Contains: angiotensin; plasminogen

C:Species: Mus musculus (house mouse)

C:Date: 20-Sep-1991 #sequence revision 01-Nov-1996 #text_change 18-Jun-1999

C:Accession: A38514; S48202; S48203

R:Deegen, S. J. F.; Bell, S. M.; Schaefer, L. A.; Elliott, R. W.
Genomics 8, 49-61, 1990

A:Title: Characterization of the cDNA coding for mouse plasminogen and localization of t

A:Reference number: A38514; MUID:91184812

A:Accession: A38514

A:Molecule type: mRNA

A:Residues: 1-812 <RGS>

A:Cross-references: GB:J04766; NID:q200402; PIDN:AAA50168.1; PID:q200403

R:Iljin, H. R.; van Hoel, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994

A:Title: Characterization of the murine plasma fibrinolytic system.
A:Reference number: S48202; MUID:95010076

A:Accession: S48202

A:Molecule type: protein

A:Residues: 20-25 <LIJ>

A:Accession: S48203

A:Molecule type: protein

A:Residues: 22-27 <LI2>

C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many
C:Comment: plasminogen is converted into plasmin by plasminogen activators, both plas
mediately after dissociation from the clot. In the presence of the inhibitor, the act
e inhibitor, the activation involves also removal of the activation peptide.
C:Comment: Stromelysin 1 (see PIR:KCMS1) acts on plasminogen to produce angiotensin.
eul in treating solid tumors.
C:Function:

A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a
us the walls of the graafian follicle; also activates the urokinase-type plasminogen

A:Pathway: fibrinolysis

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol

C:Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; h

F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-812/Product: plasminogen #status predicted <PRO>

F:20-96/Domain: activation peptide #status predicted <APT>

F:79-466/Product: angiotensin #status predicted <AST>

F:97-581,582-812/Product: plasmin #status predicted <MAT>

F:97-581/Domain: chain A #status predicted <ACH>

F:103-181/Domain: kringle homology <KR1>

F:185-262/Domain: kringle homology <KR2>

F:275-352/Domain: kringle homology <KR3>

F:377-454/Domain: kringle homology <KR4>

F:481-560/Domain: kringle homology <KR5>

F:582-812/Domain: chain B #status predicted <BCB>

F:582-803/Domain: trypsin homology <TRY>

F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335
bonds: #status predicted

F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted

F:136,308/Binding site: carboxylate (Asn) (covalent) #status predicted

F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted

F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental

F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 92.8%; Score 128; DB 1; Length 812;
Best Local Similarity 91.3%; Pred. No. 1.2e-10;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNPDDVGGMATYTNPKRLDY 23
|||||
Db 532 RNPDDVGGMATYTNPKRLDY 554

RESULT 4

plasmin (EC 3.4.21.7) precursor - sheep (fragments)

N:Alternate names: plasminogen

N:Contains: miniplasminogen

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 28-Oct-1994 #sequence revision 01-Nov-1996 #text_change 17-Mar-1999

C:Accession: B61545; S28200

R:Schaller, J.; Rickli, E. E.
Enzyme 40, 63-69, 1988

A:Title: Structural aspects of the plasminogen of various species.
A:Reference number: A61545; MUID:89005015

A:Accession: B61545

A:Molecule type: protein

A:Residues: 1-37;38-117 <SCH>

R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E. E.

Protein Seq. Data Anal. 5, 21-25, 1992
 A:Title: Complete amino acid sequence of ovine miniplasminogen.
 A:Reference number: S28200; MUID:93149995
 A:Accession: S28200
 A:Molecule type: protein
 A:Residues: 118-460 <S2>
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; 2
 F:1-37/38-117,118-460/Product: plasminogen (fragments) #status experimental <PRO>
 F:1-37/Domain: activation peptide (fragment) #status experimental <APT>
 F:38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT>
 F:411-118/Domain: kringle homology <KR4>
 F:118-460/Product: miniplasminogen #status experimental <MIN>
 F:132-211/Domain: kringle homology <KR5>
 F:226-460/Domain: plasmin chain B #status experimental <BCH>
 F:231-453/Domain: trypsin homology <TRY>
 F:272,315,410/active site: His, Asp, Ser #status predicted

Query Match 89.9%; Score 124; DB 2; Length 460;
 Best Local Similarity 87.0%; Pred. No. 2,6e-10;
 Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNPDDGVGPMAYTTPKRLDY 23
 Db 183 RNPDDGVNGPMCTTPKRLFDY 205

RESULT 5
 146260
 Plasmin (EC 3.4.21.7) precursor - western European hedgehog
 C:Species: Erinaceus europaeus (western European hedgehog)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C:Accession: 146260
 R:Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong
 J. Biol. Chem. 270, 24004-24009, 1995
 A:Title: The recurring evolution of lpa(a): Insights from cloning of hedgehog apolipoprotein
 A:Reference number: 146259; MUID:96025778
 A:Accession: 146260
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-810 <LAW>
 A:Cross-references: EMBL:U33171; NID:q1046360; PTD:q1046361
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: hydrolase; serine proteinase
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>
 F:103-181/Domain: kringle homology <KR1>
 F:185-262/Domain: kringle homology <KR2>
 F:275-352/Domain: kringle homology <KR3>
 F:379-456/Domain: kringle homology <KR4>
 F:482-561/Domain: kringle homology <KR5>
 F:582-803/Domain: trypsin homology <TRY>

Query Match 87.0%; Score 120; DB 2; Length 810;
 Best Local Similarity 82.6%; Pred. No. 1,8e-09;
 Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RNPDDGVGPMAYTTPKRLDY 23
 Db 533 RNPDDGANGPMCTTPKRLFDY 555

RESULT 6
 S00657
 Apolipoprotein(a) (EC 3.4.21.-) precursor [validated] - human
 N:Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-2000
 C:Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286
 R:McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, G.M.; Scan
 Nature 330, 132-137, 1987
 A:Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
 A:Reference number: S00657; MUID:88039109
 A:Accession: S00657

A:Molecule type: mRNA
 A:Residues: 1-4548 <MCCL>
 A:Cross-references: GB:X06690; EMBL:X06696; NID:q28619; PTD:CAA29618.1; PID:q28620
 R:Eaton, D.L.; Fless, G.M.; Kohn, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R
 Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
 A:Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous
 A:Reference number: A28017; MUID:87204109
 A:Accession: A28017
 A:Molecule type: protein
 A:Residues: 20-21,'P',22-34,'177-179','N',181-186,'T',188-196,'DKG',200-292-314,'W',316
 X',4396-4401 <EAT>
 R:Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Schwartz
 Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
 A:Title: 5' control regions of the apolipoprotein(a) gene and members of the related
 A:Reference number: A47277; MUID:93165698
 A:Accession: A47277
 A:Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <RES>
 A:Cross-references: GB:U07899; NID:q967973; PTD:q967974
 R:Malgaretti, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sa
 Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
 A:Title: Characterization by yeast artificial chromosome cloning of the linked apolip
 A:Reference number: A47233; MUID:93087573
 A:Accession: 160906
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <RE2>
 A:Cross-references: GB:M90078; NID:q178786; PTD:AAA3547.1; PID:9553188
 A:Note: apo(a) gene 1 (nomenclature of reference 152415)
 A:Accession: A47233
 A:Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <RE5>
 A:Cross-references: GB:M90079; NID:q178784; PTD:AAA3546.1; PID:9553187
 R:Ichinose, A.
 Biochemistry 31, 3113-3118, 1992
 A:Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated
 A:Reference number: 152415; MUID:92207924
 A:Accession: 152415
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <KR3>
 A:Cross-references: GB:M86877; NID:q178780; PTD:AAA49909.1; PID:9553185
 A:Note: apo(a) gene 1 (nomenclature of reference 152415)
 A:Accession: 165286
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-16 <RE4>
 A:Cross-references: GB:M86878; NID:q178782; PTD:AAA51749.1; PID:9553186
 C:Genetics:
 A:Gene: GDB:LPA
 A:Cross-references: GDB:120699; OMIM:152200
 A:Map position: 6q26-6q27
 A:Note: several genes closely linked on chromosome 6 are identical in the first codin
 rs of kringle repeats
 C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
 C:Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-4548/Product: apolipoprotein(a) #status experimental <MAT>
 F:28-105/Domain: kringle homology <KR1>
 F:142-219/Domain: kringle homology <KR2>
 F:256-333/Domain: kringle homology <KR3>
 F:370-447/Domain: kringle homology <KR4>
 F:484-561/Domain: kringle homology <KR5>
 F:598-675/Domain: kringle homology <KR6>
 F:712-789/Domain: kringle homology <KR7>
 F:826-903/Domain: kringle homology <KR8>
 F:940-1017/Domain: kringle homology <KR9>
 F:1054-1131/Domain: kringle homology <KR10>
 F:1168-1245/Domain: kringle homology <KR11>
 F:1282-1359/Domain: kringle homology <KR12>
 F:1396-1473/Domain: kringle homology <KR13>

F:1510-1587/Domain: kringle homology <KR14>
 F:1624-1701/Domain: kringle homology <KR15>
 F:1738-1815/Domain: kringle homology <KR16>
 F:1852-1929/Domain: kringle homology <KR17>
 F:1966-2043/Domain: kringle homology <KR18>
 F:2080-2157/Domain: kringle homology <KR19>
 F:2194-2271/Domain: kringle homology <KR20>
 F:2308-2385/Domain: kringle homology <KR21>
 F:2422-2499/Domain: kringle homology <KR22>
 F:2536-2613/Domain: kringle homology <KR23>
 F:2650-2727/Domain: kringle homology <KR24>
 F:2764-2841/Domain: kringle homology <KR25>
 F:2878-2955/Domain: kringle homology <KR26>
 F:2992-3069/Domain: kringle homology <KR27>
 F:3106-3183/Domain: kringle homology <KR28>
 F:3220-3297/Domain: kringle homology <KR29>
 F:3334-3411/Domain: kringle homology <KR30>
 F:3448-3525/Domain: kringle homology <KR31>
 F:3562-3639/Domain: kringle homology <KR32>
 F:3676-3753/Domain: kringle homology <KR33>
 F:3782-3859/Domain: kringle homology <KR34>
 F:3896-3973/Domain: kringle homology <KR35>
 F:4010-4087/Domain: kringle homology <KR36>
 F:4124-4201/Domain: kringle homology <KR37>
 F:4228-4307/Domain: kringle homology <KR38>
 F:4328-4541/Domain: trypsin homology <TRY>

Query Match

Best Local Similarity 84.8%; Score 117; DB 1; Length 4548;
 Best Local Similarity 78.3%; Pred. No. 3,36-08;
 Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNPDDVGPMWYTTNPKRLDY 23
 DB 4279 RNPDDGNGPCWYTNPKRLFDY 4301

RESULT 7
 A61545
 Plasmn (EC 3.4.21.7) precursor - horse (fragments)

N:Alternate names: plasminogen
 N:Contains: miniplasminogen
 C:Species: Equus caballus (domestic horse)
 C:Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
 C:Accession: A61545; S17527
 R:Schaller, J.; Rickli, E.E.
 Enzyme 40, 63-69, 1988
 A:Title: Structural aspects of the plasminogen of various species.
 A:Reference number: A61545; MUID:89005015
 A:Accession: A61545
 A:Molecule type: protein
 A:Residues: 1-33,34-117 <SCH>
 R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
 Protein Seq. Data Anal. 4, 69-74, 1991
 A:Title: Complete amino acid sequence of equine miniplasminogen.
 A:Reference number: S17527; MUID:92052077
 A:Accession: S17527

A:Molecule type: protein
 A:Residues: 118-455 <SC2>
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; Z
 F:1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <PRO>
 F:1-33/Domain: activation peptide (fragment) #status experimental <APT>
 F:1-33-117,118-225,226-455/Product: plasmin (fragments) #status experimental <MAT>
 F:37-114/Domain: kringle homology <KR4>
 F:118-455/Product: miniplasminogen #status experimental <MIN>
 F:126-205/Domain: kringle homology <KR5>
 F:226-455/Domain: plasmin chain B #status experimental <BCH>
 F:226-448/Domain: trypsin homology <TRY>
 F:267,310,405/Active site: His, Asp, Ser #status predicted

Query Match 82.6%; Score 114; DB 2; Length 455;
 Best Local Similarity 78.3%; Pred. No. 7,4e-09;
 Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNPDDVGPMWYTTNPKRLDY 23
 DB 177 RNPDDGNGPCWYTNPKRLFDY 199

RESULT 8

PLRG
 plasmin (EC 3.4.21.7) precursor - pig (fragment)

N:Alternate names: plasminogen
 N:Contains: miniplasminogen
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
 C:Accession: S03733; S03737; A25834
 R:Schaller, J.; Marti, T.; Roesseler, S.J.; Kaempfer, U.; Rickli, E.E.
 Fibrinolysis 1, 91-102, 1987
 A:Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the
 A:Reference number: S03733
 A:Accession: S03733
 A:Molecule type: protein
 A:Residues: 1-560 <SCH>
 R:Brundis, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg,
 Eur. J. Biochem. 114, 465-470, 1981
 A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of huma
 A:Reference number: S03735; MUID:81212097
 A:Accession: S03737
 A:Molecule type: protein
 A:Residues: 1-57 <BRD>
 R:Brundis, R.A.; Schaller, J.; Rickli, E.E.
 Eur. J. Biochem. 149, 279-285, 1985
 A:Title: Determination of the complete amino-acid sequence of porcine miniplasminogen
 A:Reference number: A25834; MUID:85203907
 A:Accession: A25834

A:Molecule type: protein
 A:Residues: 450-790 <MAR>
 A:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a
 as the walls of the graafian follicle; also activates the urokinase-type plasminogen
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine pr
 F:1-790/Product: plasminogen #status predicted <PRO>
 F:1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLRH>
 F:1-77/Domain: activation peptide #status predicted <APT>
 F:78-560/Product: plasmin chain A #status predicted <ACH>
 F:84-162/Domain: kringle homology <KR1>
 F:166-243/Domain: kringle homology <KR2>
 F:256-333/Domain: kringle homology <KR3>
 F:358-435/Domain: kringle homology <KR4>
 F:450-790/Product: miniplasminogen #status experimental <MIN>
 F:461-540/Domain: kringle homology <KR5>
 F:561-790/Product: plasmin chain B #status experimental <BCH>
 F:561-783/Domain: trypsin homology <TRY>
 F:30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,
 bonds: #status predicted
 F:602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 81.9%; Score 113; DB 1; Length 790;
 Best Local Similarity 78.3%; Pred. No. 1,9e-08;
 Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNPDDVGPMWYTTNPKRLDY 23
 DB 512 RNPDDGNGPCWYTNPKRLFDY 534

RESULT 9

PLBO
 plasmin (EC 3.4.21.7) precursor - bovine

N:Alternate names: plasminogen
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1987 #sequence_revision 28-Apr-1995 #text_change 18-Jun-1999
 C:Accession: S45046; A25835; I45961; S03736

R.Berglund, L.; Andersen, M.D.; Petersen, T.E. submitted to the EMBL Data Library, May 1994
 A:Description: Cloning and characterization of the bovine plasminogen CDNA.
 A:Reference number: S45046
 A:Accession: S45046
 A:Molecule type: mRNA
 A:Residues: 1-812 <BER>
 A:Cross-references: EMBL:X79402; NID:G494962; PIDN:CA55939.1; PID:G494963
 A:Experimental source: liver
 A:Note: It is uncertain whether Met-1 or Met-8 is the initiator
 R.Schaller, J.; Moser, P.W.; Danneberg-Muller, G.A.K.; Rosselet, S.J.; Kamfer, U.; Rick
 Eur. J. Biochem. 149, 267-276, 1985
 A:Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plas
 A:Reference number: A25835; MUID:85203906
 A:Accession: A25835
 A:Molecule type: protein
 A:Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
 R.Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
 Biochemistry 23, 4243-4250, 1984
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for human and
 A:Reference number: I45961; MUID:85023311
 A:Accession: I45961
 A:Status: translated from GR/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 706-743, 'R', 745-812 <MAL>
 A:Cross-references: GB:K02935; NID:G163551; PIDN:AAA30714.1; PID:G163552
 R.Brundish, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
 Eur. J. Biochem. 114, 465-470, 1981
 A:Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,
 A:Reference number: S03735; MUID:81212097
 A:Accession: S03735
 A:Molecule type: protein
 A:Residues: 27-83

 A:Function:
 C:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 as the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 C:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringie homology; plasminogen-related protein precursor homology
 C:Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringie; plasma;
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:8-103/Domain: plasminogen-related protein precursor homology <PRO>
 F:27-812/Product: plasminogen #status experimental <PRO>
 F:27-103/Domain: activation peptide #status experimental <AP>
 F:104-583/Domain: plasmin #status experimental <MA>
 F:104-583/Domain: plasmin #status experimental <MA>
 F:110-188/Domain: kringie homology <KR1>
 F:192-269/Domain: kringie homology <KR2>
 F:282-359/Domain: kringie homology <KR3>
 F:384-461/Domain: kringie homology <KR4>
 F:485-564/Domain: kringie homology <KR5>
 F:584-812/Domain: plasmin chain B #status experimental <BCH>
 F:584-805/Domain: trypsin homology <TRY>
 F:56-80, 60-68, 110-188, 131-171, 159-183, 192-269, 195-323, 213-252, 241-264, 282-359, 303-342, 33
 bonds: #status predicted
 F:315/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:365/Binding site: carboxylate (Ser) (covalent) #status experimental
 F:624, 667, 762/Active site: His, Asp, Ser #status predicted
 Query Match 80.4%; Score 111; DB 1; Length 812;
 Best Local Similarity 78.3%; Pred. No. 3, 8e-08;
 Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 RNPDCVCGPMAYTTPRKLYD 23
 Db 536 RNPDCVCGPMAYTTPRKLYD 558
 RESULT 10
 JC5061
 macrophage-stimulating protein 1 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Jan-1997 #sequence-revision 31-Jan-1997 #text-change 16-Jun-2000
 C:Accession: JC5061

R.Oshiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takasu
 Biochem. Biophys. Res. Commun. 227, 273-280, 1996
 A:Title: Molecular cloning of rat macrophage-stimulating protein and its involvement
 A:Reference number: JC5061; MUID:97011126
 A:Accession: JC5061
 A:Molecule type: mRNA
 A:Residues: 1-716 <OH>
 A:Cross-references: EMBL:X95096; NID:G1669718; PIDN:CAA64473.1; PID:G1669719
 C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C:Superfamily: hepatocyte growth factor; kringie homology; trypsin homology
 C:Keywords: duplication; glycoprotein; growth factor; kringie
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-488/488-716/Product: macrophage-stimulating protein 1 #status predicted <MA>
 F:32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>
 F:110-186/Domain: kringie homology <KR1>
 F:191-268/Domain: kringie homology <KR2>
 F:292-370/Domain: kringie homology <KR3>
 F:379-457/Domain: kringie homology <KR4>
 F:489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>
 F:489-709/Domain: trypsin homology <TRY>
 F:772,305,620/Binding site: carboxylate (Asn) (covalent) #status predicted
 Query Match 68.1%; Score 94; DB 1; Length 716;
 Best Local Similarity 65.2%; Pred. No. 1e-05;
 Matches 15; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 RNPDCVCGPMAYTTPRKLYD 23
 Db 429 RNPDCVCGPMAYTTPRKLYD 451
 RESULT 11
 A47136
 macrophage-stimulating protein 1 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 #sequence-revision 14-Nov-1997 #text-change 18-Jun-1999
 C:Accession: A40331; MUID:92002016
 R.Han, S.; Stuart, L.A.; Degen, S.J.F.
 Biochemistry 30, 9768-9780, 1991
 A:Title: Characterization of the DNFI52 locus on human chromosome 3: identification
 A:Reference number: A40331; MUID:92002016
 A:Accession: A40331
 A:Molecule type: DNA
 A:Residues: 1-711 <HA>
 A:Cross-references: GB:M74179
 A:Accession: B40331
 A:Molecule type: mRNA
 A:Residues: 1-711 <HA2>
 A:Cross-references: GB:M74178; NID:G183976; PIDN:AAA50165.1; PID:G183977
 R.Yoshimura, T.; Yuhki, N.; Wang, M.H.; Skeel, A.; Leonard, E.J.
 J. Biol. Chem. 268, 15461-15468, 1993
 A:Title: Cloning, sequencing, and expression of human macrophage stimulating protein
 A:Reference number: A47136; MUID:93340141
 A:Accession: A47136
 A:Molecule type: mRNA
 A:Residues: 1-12, 'C', 14-622, 'F', 624-711 <YOS>
 A:Cross-references: GB:I11924; NID:G398037; PIDN:AAA59872.1; PID:G398038
 A:Note: authors translated the codon TTT for residue 623 as Leu; parts of this sequen
 R.Skeel, A.; Yoshimura, T.; Snowalter, S.D.; Tanaka, S.; Appella, E.; Leonard, E.J.
 J. Exp. Med. 173, 1227-1234, 1991
 A:Title: Macrophage stimulating protein: purification, partial amino acid sequence, a
 A:Reference number: A61395; MUID:91217635
 A:Accession: A61395
 A:Molecule type: protein
 A:Residues: 230-247, 288-291, 'E', 293-295, 'X', 297-301, 'X', 303, 'E', 305, 'EX', 308-310, 326-
 A:Experimental source: plasma
 A:Genetics:
 C:Gene: GDB:MS1; D3F15S2; DNFI5S2; HGFL
 A:Cross-references: GDB:128833; OMIM:142408
 A:Map position: 3p21-3p21.3
 C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C:Superfamily: hepatocyte growth factor; kringie homology; trypsin homology
 C:Keywords: duplication; glycoprotein; growth factor; kringie; plasma

F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-483/484-711/Product: macrophage-stimulating protein 1 #status predicted <MAT>
 F:19-483/Domain: alpha chain #status predicted <ACH>
 F:110-186/Domain: kringle homology <KR1>
 F:191-268/Domain: kringle homology <KR2>
 F:283-361/Domain: kringle homology <KR3>
 F:370-448/Domain: kringle homology <KR4>
 F:484-711/Domain: beta chain #status predicted <BCH>
 F:484-704/Domain: trypsin homology <TRY>
 F:56-78,60-66,110-186,131-169,157-181,191-268,212-251,240-263,283-361,304-343,332-355,37
 F:72,296,615/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.7%; Score 92; DB 1; Length 711;
 Best Local Similarity 65.2%; Pred. No. 2e-05;
 Matches 15; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RNPDDVGSPMAVYTNPRKLYDY 23
 DB 420 RNPDDSHGPMWCTMDPRPFY 442

RESULT 12

A:Accession: A40332
 macrophage-stimulating protein 1 precursor - mouse
 N:Alternate names: hepatocyte growth factor-like protein
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1999
 C:Accession: A40332; #sequence_revision 17-Jul-1992 #text_change 18-Jun-1999
 C:Accession: A40332; B40332
 R:Begeen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
 Biochemistry 30: 9781-9791, 1991
 A:Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth fact
 A:Reference number: A40332; MUID:92002017
 A:Accession: A40332
 A:Molecule type: DNA
 A:Residues: 1-716 <DEG>
 A:Cross-references: GB:M74180; NID:g193831; PIDN:AAA50166.1; PID:g193832
 A:Accession: B40332
 A:Molecule type: mRNA
 A:Residues: 1-18; 'P', 20-716 <DEG2>
 A:Cross-references: GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g193834
 C:Genetics:
 A:Insertions: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 47
 C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
 C:Keywords: duplication; glycoprotein; growth factor; kringle
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:19-488,489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>
 F:19-483/Domain: alpha chain #status experimental <ACH>
 F:110-186/Domain: kringle homology <KR1>
 F:191-268/Domain: kringle homology <KR2>
 F:292-370/Domain: kringle homology <KR3>
 F:379-457/Domain: kringle homology <KR4>
 F:484-711/Domain: beta chain #status experimental <BCH>
 F:489-709/Domain: trypsin homology <TRY>
 F:72,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 65.2%; Score 90; DB 1; Length 716;
 Matches 15; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RNPDDVGSPMAVYTNPRKLYDY 23

DB 429 RNPDDSHGPMWCTMDPRPFY 442

RESULT 13

A:Accession: A35644
 hepatocyte growth factor precursor - rat
 N:Alternate names: hepatoleitin A; scatter factor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 21-Jul-2000
 C:Accession: A35644; S13211
 R:Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimizu, S.; Nakamura

Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990

A:Title: Deduced primary structure of rat hepatocyte growth factor and expression of
 A:Reference number: A35644; MUID:90222197
 A:Accession: A35644
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-728 <TAS>
 A:Cross-references: GB:D90102; GB:M32987; NID:g220766; PIDN:BAAL4133.1; PID:g220767
 A:Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 4
 R:Okajima, A.; Miyazawa, K.; Kitamura, N.
 Eur. J. Biochem. 193, 375-381, 1990
 A:Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA
 A:Reference number: S13211; MUID:91031482
 A:Accession: S13211
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-728 <OKA>
 A:Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
 C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C:Function:
 A:Description: stimulates mitosis of hepatocytes and other cells
 A:Note: does not have proteinase activity
 A:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
 C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle;

F:1-32/Domain: signal sequence #status predicted <SIG>
 F:56-495/Product: hepatocyte growth factor #status predicted <MAT>
 F:56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
 F:129-207/Domain: kringle homology <KR1>
 F:212-289/Domain: kringle homology <KR2>
 F:306-384/Domain: kringle homology <KR3>
 F:392-470/Domain: kringle homology <KR4>
 F:496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
 F:496-719/Domain: trypsin homology <TRY>
 F:33/Modified site: pyrroline carboxylic acid (Gln) (in mature form) #status predic
 F:293,403,566,656/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:488-607/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 59.4%; Score 82; DB 1; Length 728;
 Matches 14; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 RNPDDVGSPMAVYTNPRKLYDY 23

DB 442 RNPDDSHGPMWCTMDPRPFY 442

RESULT 14

A:Accession: JH0579
 hepatocyte growth factor precursor [validated] - human
 N:Alternate names: hepatoleitin A; scatter factor
 C:Species: Homo sapiens (man)
 C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
 C:Accession: JH0579; JH0333; A41140; B36677; A35512; A39006; PH0114; A37796;
 R:Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.
 Gene 102, 213-219, 1991
 A:Title: Organization of the human hepatocyte growth factor-encoding gene.
 A:Accession number: JH0579; MUID:91340155
 A:Accession: JH0579
 A:Molecule type: DNA
 A:Residues: 1-728 <SEK>
 A:Cross-references: DDBJ:D90318
 A:Note: the authors translated the codon GAA for residue 662 as Gly
 R:Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.
 submitted to JIPD, March 1991
 A:Description: Organization of the human hepatocyte growth factor-encoding gene.
 A:Reference number: JH0333
 A:Accession: JH0333
 A:Molecule type: DNA
 A:Residues: 1-481; 'R', 484-728 <SEK2>
 R>Weidner, K.M.; Arakaki, N.; Hartman, G.; Vandekerckhove, J.; Weingart, S.; Rieder,
 Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
 A:Title: Evidence for the identity of human scatter factor and human hepatocyte growth
 A:Reference number: A41140; MUID:91334393

A:Accession: A41140
 A:Molecule type: mRNA
 A:Residues: 1-728 <MT>
 A:Cross-references: GB:M73239; NID:g337935; PIDN:AAA64239.1; PID:g337936
 R:Seiki, T.; Ihara, I.; Sugimura, A.; Shimomishi, M.; Nishizawa, T.; Asami, O.; Hagiya, N
 Biochem. Biophys. Res. Commun. 172, 321-327, 1990
 A:Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor
 A:Reference number: A36677; MUID:91025062
 A:Accession: B36677
 A:Molecule type: mRNA
 A:Residues: 1-728 <SE3>
 A:Cross-references: GB:M60718; NID:g184031; PIDN:AAA52648.1; PID:g184032
 A:Accession: A36677
 A:Molecule type: mRNA
 A:Residues: 1-161,167-728 <SE4>
 A:Cross-references: EMBL:X16323
 A:Experimental source: leukocyte
 R:Miyaizawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
 Biochem. Biophys. Res. Commun. 163, 967-973, 1989
 A:Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fac
 A:Reference number: A33512; MUID:89392017
 A:Accession: A33512
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-728 <MT>
 A:Cross-references: GB:M29145; NID:g184041; PIDN:AAA52650.1; PID:g306846
 R:Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hitz
 Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
 A:Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy
 A:Reference number: A39006; MUID:9110540
 A:Accession: A39006
 A:Molecule type: mRNA
 A:Residues: 1-161,167-728 <RUB>
 A:Cross-references: GB:M55379
 A:Experimental source: embryonic lung
 R:Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirose, S.; Kondo, J.; Nakayama,
 Biochem. Biophys. Res. Commun. 175, 660-667, 1991
 A:Title: Identification of the N-terminal residue of the heavy chain of both native and
 A:Reference number: PH0114; MUID:91207365
 A:Accession: PH0114
 A:Molecule type: protein
 A:Residues: 32-43;53-58 <YOS>
 A:Experimental source: Plasma
 R:Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
 J. Cell Biol. 111, 2097-2108, 1990
 A:Title: Scatter factor: molecular characteristics and effect on the invasiveness of epi
 A:Reference number: A37796; MUID:91035621
 A:Accession: A37796
 A:Molecule type: protein
 A:Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'X',
 R:Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimomishi, M.; Sugimura, A.; Tash
 Nature 342, 440-443, 1989
 A:Title: Molecular cloning and expression of human hepatocyte growth factor.
 A:Reference number: S06794; MUID:90066676
 A:Accession: S06794
 A:Molecule type: mRNA
 A:Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'W',301-316,'A',318-335,'K',337-386,'
 A:Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
 A:Experimental source: liver
 A:Note: the authors translated the codon CAG for residue 727 as Glu
 R:Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchm
 Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
 A:Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact
 A:Reference number: I59214; MUID:93087571
 A:Accession: I59214
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-288,'ET' <HAR>
 A:Cross-references: GB:I02931; NID:g184033; PIDN:AAA52649.1; PID:g184034
 R:Miyaizawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
 Eur. J. Biochem. 197, 15-22, 1991
 A:Title: An alternatively processed mRNA generated from human hepatocyte growth factor g

A:Reference number: S15443; MUID:91200041
 A:Accession: S15443
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-288,'ET' <MTY2>
 A:Cross-references: EMBL:X57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
 R:Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
 Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
 A:Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: clon
 A:Reference number: I52253; MUID:92062058
 A:Accession: I52253
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 161-166 <SHU>
 A:Cross-references: GB:S62561; NID:g237996; PIDN:AAB20169.1; PID:g237997
 A:Gene: GDB:HGF
 A:Cross-references: GDB:I27524; OMIM:142409
 A:Map position: 7921.1-7921.1
 A:introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1;
 C:complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C:function:
 A:Description: stimulates mitosis of hepatocytes and other cells
 A:Note: does not have proteinase activity
 C:Superfamily: hepatocyte growth factor; kinkle homology; trypsin homology
 C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kinkle;
 F:1-31/Domain: signal sequence #status predicted <SI>
 F:32-494/Domain: signal sequence #status predicted <SI>
 F:32-494/Domain: alpha chain #status experimental <ACH>
 F:128-206/Domain: kinkle homology <KR1>
 F:211-288/Domain: kinkle homology <KR2>
 F:305-383/Domain: kinkle homology <KR3>
 F:391-469/Domain: kinkle homology <KR4>
 F:495-728/Domain: beta chain #status experimental <BCH>
 F:495-716/Domain: trypsin homology <TRY>
 F:32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi
 F:294,402,566,653/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:487-604/Disulfide bonds: #status predicted

Query Match 58.7%; Score 81; DB 1; Length 728;
 Best Local Similarity 60.9%; Pred. No. 0.00084;
 Matches 14; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 QY 1 RNPDVGCPAAATYTNPRKLYDY 23
 DB 441 RNPDDAHGRCYCTGNLIPWDY 463

RESULT 15
 A60185
 hepatocyte growth factor precursor - mouse
 N:Alternate names: hepatietin A; scatter factor
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Mar-1993 #sequence revision 26-May-1994 #text change 16-Jun-2000
 C:Accession: J02117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758; J00231
 R:Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
 Biochem. Biophys. Res. Commun. 199, 772-779, 1994
 A:Title: Identification of mouse mammary fibroblast-derived mammary growth factor as
 A:Reference number: J02117; MUID:94183257
 A:Accession: J02117
 A:Molecule type: mRNA
 A:Residues: 1-728 <SAS2>
 A:Cross-references: GB:DI0212; NID:g220435; PIDN:BAA01064.1; PID:g220436
 A:Experimental source: fibroblast, Cos-1 cell
 A:Note: submitted to JIPID, May 1993
 A:Accession: PC2064
 A:Molecule type: protein
 A:Residues: 496-504 <SAS2>
 R:Nosen, E.M.; Meromsky, L.; Setler, E.; Winter, D.W.; Goldberg, I.D.
 Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990
 A:Title: Purified scatter factor stimulates epithelial and vascular endothelial cell
 A:Reference number: A60185; MUID:90377927
 A:Accession: A60185

RESULT 21

S10511

thrombin (EC 3.4.21.5) B chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 22-Jun-1999

C:Accession: S10511; A60576; B42696

R:Idmanich, M.; Monard, D.

Nucleic Acids Res. 18, 4251, 1990

A:Title: cDNA sequence of rat prothrombin.

A:Reference number: S10511; MUID:90332426

A:Accession: S10511

A:Molecule type: mRNA

A:Residues: 1-617 <DIR>

A:Cross-references: EMBL:X52835; NID:956569; PIDN:CA37017.1; PID:956970

R:Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.

Endocrinology 126, 167-175, 1990

A:Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.

A:Reference number: A60576; MUID:90091942

A:Accession: A60576

A:Molecule type: protein

A:Residues: 44-58 <HEN>

A:Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute

R:Banfield, D.K.; Macgillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992

A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq

A:Reference number: A42696; MUID:92212913

A:Accession: B42696

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 383-617/'E' <BAN>

A:Cross-references: GB:M81397

C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology

C:Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hyd

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-43/Domain: propeptide #status predicted <PRO>

F:28-88/Domain: Gla domain homology <GLA>

F:44-617/Product: prothrombin #status experimental <PMAT>

F:109-187/Domain: kringle homology <KR1>

F:215-292/Domain: kringle homology <KR2>

F:360-609/Domain: trypsin homology <TRY>

F:50-51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxylglutamic acid (Glu) #stat

F:61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5

F:402,458,564/Active site: His, Asp, Ser #status predicted

Query Match

Best local Similarity 52.9%; Score 73; DB 2; Length 617;

Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNPDCGVGPWATYTP 17

DB 159 RNPDSSTGPMCTYTP 175

RESULT 22

T18518

apolipoprotein(a) - western European hedgehog (fragment)

C:Species: Erinaceus europaeus (western European hedgehog)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999

C:Accession: T18518

R:Lawn, R.M.; Boommark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong

J. Biol. Chem. 270, 24004-24009, 1995

A:Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot

A:Reference number: I46259; MUID:96025778

A:Accession: T18518

A:Status: preliminary; translated from GB/EMBL/DBU

A:Molecule type: mRNA

A:Residues: 1-2869 <LAN>

A:Cross-references: EMBL:U33170; NID:g1046358; PID:g1046359; PIDN:AA48522.1

A:Experimental source: liver

C:Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, con

ent apolipoprotein(a).

Query Match 52.5%; Score 72.5; DB 2; Length 2869;

Best local Similarity 56.5%; Pred. No. 0.065;

Matches 13; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 1 RNPDCGVGPWATYTPPKLYDY 23

DB 2548 RNPDEGV-APMCYTTSAMRWEY 2569

RESULT 23

A35827

thrombin (EC 3.4.21.5) B chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 22-Jun-1999

C:Accession: A35827; A42696; S12081

R:Deegen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pal, J

DNA Cell Biol. 9, 487-498, 1990

A:Title: Characterization of the cDNA coding for mouse prothrombin and localization o

A:Reference number: A35827; MUID:91025551

A:Accession: A35827

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-618 <DEC>

A:Cross-references: GB:X52308; NID:g53813; PIDN:CA36548.1; PID:g53814

A:Experimental source: strain C57BL/6

A:Note: the data were obtained from females resulting from the cross of M. domesticus

R:Banfield, D.K.; Macgillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992

A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and

A:Reference number: A42696; MUID:92212913

A:Accession: A42696

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 384-618/'E' <BAN>

A:Cross-references: GB:M81394

C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology

C:Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; h

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-43/Domain: propeptide #status predicted <PRO>

F:28-88/Domain: Gla domain homology <GLA>

F:44-618/Product: prothrombin B #status predicted <MAT>

F:109-187/Domain: kringle homology <KR1>

F:215-293/Domain: kringle homology <KR2>

F:361-610/Domain: trypsin homology <TRY>

F:50-51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxylglutamic acid (Glu) #stat

F:61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-54

F:403,459,565/Active site: His, Asp, Ser #status predicted

Query Match

Best local Similarity 51.4%; Score 71; DB 2; Length 618;

Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNPDCGVGPWATYTP 17

DB 159 RNPDSSTGPMCTYTP 175

RESULT 24

TBHU

thrombin (EC 3.4.21.5) precursor [validated] - human

N:Alternate names: coagulation factor II

N:Contains: prothrombin

C:Species: Homo sapiens (man)

C:Date: 30-Nov-1980 #sequence_revision 22-Jul-1994 #text_change 08-Dec-2000

C:Accession: A29351; A00914; B00914; A37549; A37550; I51952

R:Deegen, S.J.F.; Davie, E.W.

Biochemistry 26, 6165-6177, 1987

A:Title: Nucleotide sequence of the gene for human prothrombin.

A:Reference number: A29351; MUID:88077877

A:Accession: A29351

A:Molecule type: DNA

A:Residues: 1-622 <DEG>

A:Cross-references: GB:M17262; GB:M33691; NID:g558069; PIDN:AA63054.1; PID:g339641

R:Deegen, S.J.F.; Macgillivray, R.T.A.; Davie, E.W.

Biochemistry 22, 2087-2097, 1983
 A:Title: Characterization of the complementary deoxyribonucleic acid and gene coding for
 A:Reference number: A00914; MUID:83231469
 A:Accession: A00914
 A:Molecule type: mRNA
 A:Residues: 8-163, 'N', 165-622 <DE2>
 A:Cross-references: GB:Y00595; GB:J00307; NID:g37128; PIDN:CAA23842.1; PID:g1335344
 A:Accession: B00914
 A:Molecule type: DNA
 A:Residues: 188-311 <DE3>
 A:Walz, D.A.; Hewett-Evans, D.; Seegers, W.H.
 Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
 A:Reference number: A37549; MUID:77193964
 A:Accession: A37549
 A:Molecule type: protein
 A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'W', 196-308,
 R. Butkowski, R.J.; Elton, J.; Downing, M.R.; Mann, K.G.
 J. Biol. Chem. 252, 4942-4957, 1977
 A:Title: Primary structure of human prothrombin 2 and alpha-thrombin.
 A:Reference number: A37550; MUID:77207112
 A:Accession: A37550
 A:Molecule type: protein
 A:Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-
 J. Rablet, M.J.; Blashill, A.; Furie, B.; Furie, B.C.
 J. Biol. Chem. 261, 13210-13215, 1986
 A:Reference number: A37551; MUID:87008532
 A:Contents: annotation; activation cleavages
 R. MacGillivray, R.T.; Irwin, D.M.; Guineto, E.R.; Stone, J.C.
 Ann. N. Y. Acad. Sci. 485, 73-79, 1986
 A:Title: Recombinant genetic approaches to functional mapping of thrombin.
 A:Reference number: I51952; MUID:87182874
 A:Accession: I51952
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-2, 'R', 5-100 <RES>
 A:Cross-references: GB:M3031; NID:g190723; PIDN:AAA60220.1; PID:g190724
 C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
 C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
 C:Comment: The gamma-carboxyglutamate residues bind calcium ions, result from the carboxy
 C:Comment: The prothrombin precursor is synthesized in the liver.
 C:Genetics:
 A:Gene: GDB:F2
 A:Cross-references: GDB:11894; OMIM:176930
 A:Map position: 11p11-11q12
 A:Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C:Keywords: acute phase; blood coagulation; calcium binding; carboxylglutamic acid; dupli
 F:1-24/Domain: signal sequence #status predicted <SIS>
 F:25-43/Domain: propeptide #status predicted <PRO>
 F:28-87/Domain: Gla domain homology <GLA>
 F:44-622/Product: prothrombin #status experimental <MAT>
 F:108-186/Domain: activation peptide #status experimental <APT>
 F:213-291/Domain: kringle homology <KR1>
 F:328-363/Product: thrombin light chain #status experimental <LCH>
 F:364-622/Product: thrombin heavy chain #status experimental <HCH>
 F:364-613/Domain: trypsin homology <TRY>
 F:45,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status
 F:121,143/Binding site: carboxylate (asn) (covalent) #status predicted
 F:336-482,536-550,564-594/Disulfide bonds: #status predicted
 F:391-407/Disulfide bonds: #status experimental
 F:406/62/Active site: His, Asp #status predicted
 F:416/Binding site: carboxylate (asn) (covalent) #status experimental
 F:568/Active site: Ser #status experimental

Query Match 51.4%; Score 71; DB 1; Length 622;
 Best Local Similarity 64.7%; Pred. No. 0.021;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNPDDVGGMWATYTNP 17
 ||||| |||||
 Db 158 RNPDSSTGTGPMCTTDP 174

RESULT 25
 C61545
 plasmin (EC 3.4.21.7) precursor - goat (fragments)
 N:Alternate names: plasminogen
 C:Species: Capra aegagrus hircus (domestic goat)
 C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
 C:Accession: C61545
 R:Schaller, J.; Rickli, E.E.
 Enzyme 40, 63-69, 1988
 A:Title: Structural aspects of the plasminogen of various species.
 A:Reference number: A61545; MUID:89005015
 A:Accession: C61545
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-123 <SCH>
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
 C:Keywords: hydrolase; serine proteinase
 F:41-118/Domain: kringle homology <KR4>

Query Match 49.6%; Score 68.5; DB 2; Length 123;
 Best Local Similarity 52.2%; Pred. No. 0.0082;
 Matches 12; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 RNPDDVGGMWATYTNP 23
 ||||| |||||
 Db 91 RNPDD-KSPWCYTTPRVMEF 112

RESULT 26
 A60140
 plasmin (EC 3.4.21.7) precursor - chicken (fragment)
 N:Alternate names: plasminogen
 C:Species: Gallus gallus (chicken)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
 C:Accession: A60140
 R:Gyenes, M.; Pálffy, L.
 Biochim. Biophys. Acta 832, 326-330, 1985
 A:Title: The kringle 4 domain of chicken plasminogen.
 A:Reference number: A60140; MUID:86077796
 A:Accession: A60140
 A:Molecule type: protein
 A:Residues: 189 <GYE>
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
 F:6-83/Domain: kringle homology <KR>
 F:6-83,27-66,55-78/Disulfide bonds: #status predicted
 F:39/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 48.2%; Score 66.5; DB 2; Length 89;
 Best Local Similarity 52.2%; Pred. No. 0.011;
 Matches 12; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 RNPDDVGGMWATYTNP 23
 ||||| |||||
 Db 56 RNPDD-KSPWCYTTPRVMEF 77

RESULT 27
 A32869
 apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 22-Jun-1999
 C:Accession: A32869; A30848
 R:Tomlinson, J.E.; McLean, J.W.; Lawm, R.M.
 J. Biol. Chem. 264, 5957-5965, 1989
 A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis
 A:Reference number: A32869; MUID:89174660

A:Accession: A32869
 A:Molecule type: mRNA
 A:Residues: 1-1420 <TOM>
 A:Cross-references: GB:J04635; NID:9342072; PIDN:AAA36833.1; PID:9342073
 C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
 C:Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
 F:50-127/Domain: kringle homology <KR1>
 F:164-241/Domain: kringle homology <KR2>
 F:278-355/Domain: kringle homology <KR3>
 F:392-469/Domain: kringle homology <KR4>
 F:506-583/Domain: kringle homology <KR5>
 F:620-697/Domain: kringle homology <KR6>
 F:726-803/Domain: kringle homology <KR7>
 F:840-917/Domain: kringle homology <KR8>
 F:954-1031/Domain: kringle homology <KR9>
 F:1068-1145/Domain: kringle homology <KR10>
 F:1191-1413/Domain: trypsin homology <TRY>

Query Match 47.5%; Score 65.5; DB 2; Length 1420;
 Best Local Similarity 47.8%; Pred. No. 0.32;
 Matches 11; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
 QY 1 RNPDDVGGPMAYTTNPKRLYD 23
 DB 776 RNPDAEI-RPMCTMDPRVMEY 797

RESULT 28
 E61545
 plasmin (EC 3.4.21.7) precursor - dog (fragments)
 N:Alternate names: plasminogen
 C:Species: Canis lupus familiaris (dog)
 C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
 C:Accession: E61545
 R:Schaller, J.; Rickli, E. E.
 Enzyme 40; 63-69; 1988
 A:Title: Structural aspects of the plasminogen of various species.
 A:Reference number: A61545; MUID:89005015
 A:Accession: E61545
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-120 <SCH>
 C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C:Keywords: hydrolase; serine proteinase
 F:37-114/Domain: kringle homology <KR4>

Query Match 45.3%; Score 62.5; DB 2; Length 120;
 Best Local Similarity 47.8%; Pred. No. 0.06;
 Matches 11; Conservative 4; Mismatches 7; Indels 1; Gaps 1;
 QY 1 RNPDDVGGPMAYTTNPKRLYD 23
 DB 87 RNPDAI-KSPWCYTTPDSVAMEF 108

RESULT 29
 E70711
 hypothetical protein Rv1490 - Mycobacterium tuberculosis (strain H37Rv)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C:Accession: E70711
 R:Colet, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393; 537-544; 1998
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987
 A:Accession: E70711
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-435 <COL>
 A:Cross-references: GB:Z79701; GB:A1123456; NID:93261635; PIDN:CAB02040.1; PID:91524237

A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: Rv1490
 C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1490

Query Match 43.5%; Score 60; DB 2; Length 435;
 Best Local Similarity 47.6%; Pred. No. 0.57;
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 3 PDGDDVGGPMAYTTNPKRLYD 23
 DB 259 PHGWENPMAYATTPQRLVDY 279

RESULT 30
 B45082
 neurotrophic receptor ror2 precursor - human
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
 C:Accession: B45082
 R:Maslakowski, P.; Carroll, R. D.
 J. Biol. Chem. 267; 26181-26190; 1992
 A:Title: A novel family of cell surface receptors with tyrosine kinase-like domain.
 A:Reference number: A45082; MUID:93100347
 A:Accession: B45082
 A:Molecule type: mRNA
 A:Residues: 1-943 <MAS>
 A:Cross-references: GB:M97639; NID:9337466; PIDN:AAA60276.1; PID:9337467
 A:Note: sequence extracted from NCBI backbone (NCBI:120918)
 C:Genetics:
 A:Gene: GDB:NTRKR2
 A:Cross-references: GDB:136454
 A:Map position: 6p21-6p21
 C:Superfamily: neurotrophic receptor ror; immunoglobulin homology; kringle homology;
 C:Keywords: ATP; glycoprotein; kringle; phosphotransferase; transmembrane protein; ty
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-937/Product: neurotrophic receptor ror2 #status predicted <MAT>
 F:76-137/Domain: immunoglobulin homology <IMM>
 F:316-334/Domain: kringle homology <KR3>
 F:412-428/Domain: transmembrane #status predicted <TMN>
 F:471-753/Domain: protein kinase homology <KIN>
 F:479-487/Region: protein kinase ATP-binding motif
 F:70-188,318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 42.8%; Score 59; DB 2; Length 943;
 Best Local Similarity 56.2%; Pred. No. 1.8;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 RNPDDVGGPMAYTTN 16
 DB 366 RNPDDVGGPMAYTTN 381

RESULT 31
 A35029
 t-plasminogen activator (EC 3.4.21.68) precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A35029; A31597
 R:Feng, P.; Ohlsson, M.; Ny, T.
 J. Biol. Chem. 265; 2022-2027; 1990
 A:Title: The structure of the tPA-less rat tissue-type plasminogen activator gene. S
 A:Reference number: A35029; MUID:90130448
 A:Accession: A35029
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-559 <FEN>
 A:Cross-references: GB:M31197; NID:9207429; PIDN:AAA42261.1; PID:9207431; GB:J05226
 R:NY, T.; Leonardson, G.; Hsu, A.J.W.
 DNA 7; 671-677; 1988
 A:Title: Cloning and characterization of a cDNA for rat tissue-type plasminogen activ
 A:Reference number: A31597; MUID:89170114


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A:Accession: A31597
A:Molecule type: mRNA
A:Residues: 1-379, 'K', 381-559 <NYT>
A:Cross-references: GB:M2697, NID:9530159, PIDN:AAA1812.1, PID:9530160
C:Superfamily: tissue plasminogen activator; EGF homology; fibrinectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-17/Domain: signal sequence #status predicted <STG>
F:18-29/Domain: signal sequence #status predicted <PRO>
F:30-559/Product: t-plasminogen activator #status predicted <MAT>
F:30-308/Product: t-plasminogen activator chain A #status predicted <ACH>
F:38-75/Domain: fibrinectin type I repeat homology <LFI>
F:83-116/Domain: EGF homology <EGF>
F:124-205/Domain: kringle homology <KRI>
F:213-294/Domain: kringle homology <KR2>
F:309-559/Product: t-plasminogen activator chain B #status predicted <BCH>
F:309-553/Domain: trypsin homology <TRY>
F:38-68-66-75, 83-94, 88-105, 107-116, 124-205, 145-187, 176-200, 213-294, 234-276, 265-289, 297-4
F:149, 481/Binding site: carbohydrate (asn) (covalent) #status predicted
F:308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted
F:355, 404, 510/Active site: His, Asp, Ser #status predicted

Query Match          40.6%; Score 56; DB 1; Length 559;
Best Local Similarity 50.0%; Pred. No. 2.9;
Matches 12; Conservative 3; Mismatches 7; Indels 2; Gaps 2;

QY 1 RNPDGVGPGPWATYTPRKL-YDY 23
Db 266 RNPDD-ARPCWCHMKDKRLTWY 288

RESULT 32
A29941
t-plasminogen activator (EC 3.4.21.68) precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A29941; S48205; S48207; S48208
R:Rickles, R.J.; Darrow, A.L.; Strickland, S.
J. Biol. Chem. 263, 1563-1569, 1988
A>Title: Molecular cloning of complementary DNA to mouse tissue plasminogen activator mR
A:Reference number: A29941; MUID:88087303
A:Accession: A29941
A:Molecule type: mRNA
A:Residues: 1-559 <RIC>
A:Cross-references: GB:J03520; NID:9202109; PIDN:AAA0470.1; PID:9202110
R:LiJhen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A>Title: Characterization of the murine plasma fibrinolytic system.
A:Reference number: S48202; MUID:95010076
A:Accession: S48205
A:Molecule type: protein
A:Residues: 33-37, 'X', 39-40 <LIU>
A:Accession: S48207
A:Molecule type: protein
A:Residues: 309-316 <LI2>
A:Accession: S48206
A:Molecule type: protein
A:Residues: 33-37, 'X', 39-40 <LIN>
A:Superfamily: tissue plasminogen activator; EGF homology; fibrinectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-17/Domain: signal sequence #status predicted <STG>
F:18-29/Domain: signal sequence #status predicted <PRO>
F:30-559/Product: t-plasminogen activator #status predicted <MAT>
F:30-308/Product: t-plasminogen activator chain A #status predicted <ACH>
F:38-75/Domain: fibrinectin type I repeat homology <LFI>
F:83-116/Domain: EGF homology <EGF>
F:124-205/Domain: kringle homology <KRI>
F:213-294/Domain: kringle homology <KR2>
F:309-559/Product: t-plasminogen activator chain B #status predicted <BCH>
F:309-553/Domain: trypsin homology <TRY>
F:38-68-66-75, 83-94, 88-105, 107-116, 124-205, 145-187, 176-200, 213-294, 234-276, 265-289, 297-4
F:149, 481/Binding site: carbohydrate (asn) (covalent) #status predicted
F:308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted
F:355, 404, 510/Active site: His, Asp, Ser #status predicted

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Query Match          40.6%; Score 56; DB 1; Length 559;
Best Local Similarity 50.0%; Pred. No. 2.9;
Matches 12; Conservative 3; Mismatches 7; Indels 2; Gaps 2;

QY 1 RNPDGVGPGPWATYTPRKL-YDY 23
Db 266 RNPDD-ARPCWCHMKDKRLTWY 288

RESULT 33
T37219
probable lipoprotein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37219
R:Olliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1998
A:Reference number: 221615
A:Accession: T37219
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-153 <OLI>
A:Cross-references: EMBL:AL031514; PIDN:CAA20597.1; GSPDB:GN00070; SCODEB:SC2H4.03
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCODEB:SC2H4.03

Query Match          38.8%; Score 53.5; DB 2; Length 153;
Best Local Similarity 44.0%; Pred. No. 1.6;
Matches 11; Conservative 1; Mismatches 4; Indels 9; Gaps 1;

QY 3 PDGVDGPGWA-----YTNPR 18
Db 77 PGDGDGWAFFADGGLYWTSPR 101

RESULT 34
T25094
hypothetical protein T22A3.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T25094
R:McMurray, A.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19980
A:Accession: T25094
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-323 <WIL>
A:Cross-references: EMBL:281125; PIDN:CAB03383.1; GSPDB:GN00019; CESP:T22A3.6
A:Experimental source: clone T22A3
C:Genetics:
A:Gene: CESP:T22A3.6
A:Map position: 1
A:Introns: 104/2; 136/2; 226/3; 242/2
C:Superfamily: Caenorhabditis elegans hypothetical protein T22A3.6

Query Match          37.7%; Score 52; DB 2; Length 323;
Best Local Similarity 56.2%; Pred. No. 6.1;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 RNPDGVGPGPWATYTN 16
Db 14 RNPDKNPLGPGCYGN 29

RESULT 35
UKHUT
t-plasminogen activator (EC 3.4.21.68) precursor [validated] - human
N:Alternate names: t-PA; tissue plasminogen activator
C:Species: Homo sapiens (man)
C>Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 08-Dec-2000

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C:Accession: A94004; A23529; J050562; A93993; S02125; A91343; A93951; A91322; A54645; 160
R.N.Y. T.; Elgh, F.; Lund, B.
Proc. Natl. Acad. Sci. U.S.A. 81, 5355-5359, 1984
A:Title: The structure of the human tissue-type plasminogen activator gene: correlation
A:Reference number: A94004; MUID:84296137
A:Accession: A94004
A:Molecule type: DNA
A:Residues: 1-562 <NYT>
A:Cross-references: GB:L00141
A>Note: the codon given for residue 93 (ACC) is inconsistent with the authors' translation
R.Frieze, Degen, S.J.; Rajput, B.; Reich, E.
J. Biol. Chem. 261, 6972-6985, 1986
A:Title: The human tissue plasminogen activator gene.
A:Reference number: A23529; MUID:86196143
A:Accession: A23529
A:Molecule type: DNA
A:Residues: 1-562 <DEG>
A:Cross-references: GB:K03021; NID:9339817; PIDN:AAA98809.1; PID:9339818
R. Itagaki, Y.; Yasuda, H.; Morinaga, T.; Mitsuda, S.; Higashio, K.
Agric. Biol. Chem. 55, 1225-1232, 1991
A:Title: Purification and characterization of tissue plasminogen activator secreted by
A:Reference number: J050562; MUID:91291340
A:Accession: J050562
A:Molecule type: mRNA
A:Residues: 31-562 <ITR>
A:Cross-references: DDBJ:D01096; NID:9220128; PIDN:BA00881.1; PID:9441174
A:Experimental source: embryonic lung fibroblast IMR-90 cells
A>Note: part of this sequence, including the amino end of the mature protein, was confir
R. Pernicelli, D.; Holmes, W.E.; Kohr, W.O.; Harkins, R.N.; Vekari, G.A.; Ward, C.A.; Bennett
Nature 301, 214-221, 1983
A:Title: Cloning and expression of human tissue-type plasminogen activator cDNA in Esche
A:Reference number: A93293; MUID:83115262
A:Accession: A93293
A:Molecule type: mRNA
A:Residues: 1-562 <PEN>
A:Cross-references: GB:L00141
A:Experimental source: fetal lung cells
R. Saeki, H.; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.
Nucleic Acids Res. 16, 5695, 1988
A:Title: Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fe
A:Reference number: S02125; MUID:86262579
A:Accession: S02125
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-562 <SAS>
A:Cross-references: EMBL:X07393; NID:937243; PIDN:CAA930302.1; PID:937244
A:Experimental source: fetal lung cells
R. Kagitani, H.; Tagawa, M.; Hatanaka, K.; Ikari, T.; Saito, A.; Bando, H.; Okada, K.; Ma
FEBS Lett. 189, 145-149, 1985
A:Title: Expression in Escherichia coli of finger-domain lacking tissue-type plasminogen
A:Reference number: A91343; MUID:85285620
A:Accession: A91343
A:Molecule type: mRNA
A:Residues: 1-38, 'G', '86-433', 'E', '435-562' <KAG>
A:Experimental source: Detroit 562 cells; ATCC 138
R. Edlund, T.; Ny, T.; Ranby, M.; Hedem, L.O.; Palm, G.; Holmgren, E.; Josephson, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983
A:Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen acti
A:Reference number: A93951; MUID:83169656
A:Accession: A93951
A:Molecule type: mRNA
A:Residues: 251-358 <EDL>
A:Experimental source: melanoma cells
R. Pohl, G.; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jorvall, H.
Biochemistry 23, 3701-3707, 1984
A:Title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived an
differences.
A:Reference number: A90488; MUID:85000468
A:Contents: annotation: melanoma cells, partial sequence of residues 36-562, active and
R. Pohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jorvall, H.
FEBS Lett. 168, 29-32, 1984
A:Title: Differences between uterine and melanoma forms of tissue plasminogen activator.
A:Reference number: A91322; MUID:84158956

A:Accession: A91322
A:Molecule type: protein
A:Residues: 33-45; 311-320 <POH>
A:Experimental source: uterus
A>Note: In the uterus, cleavage of the activation peptide may also occur after 38-Gln
R. van Zonneveld, A.J.; Veerman, H.; Pannekoek, H.
J. Biol. Chem. 261, 14214-14218, 1986
A:Reference number: A37567; MUID:87033611
A:Contents: annotation: fibrin binding site
R. Verheijen, J.H.; Caspers, M.P.M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; En
EMBO J. 5, 3525-3530, 1986
A:Title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen
A:Reference number: A37568; MUID:87161761
A:Contents: annotation: fibrin binding site
R. Dodd, I.; Nunn, B.; Robinson, J.H.
Thromb. Haemost. 59, 523-528, 1988
A:Title: Isolation, identification and pharmacokinetic properties of human tissue-type
A:Reference number: A60902; MUID:89044681
A:Contents: annotation: novel forms of expressed recombinant t-PA
R. Harris, T.J.R.; Patel, T.; Marston, F.A.O.; Little, S.; Emlage, J.S.; Opdenakker, G
Mol. Biol. Med. 3, 279-292, 1986
A:Title: Cloning of cDNA coding for human tissue-type plasminogen activator and its e
A:Reference number: A54645; MUID:86284200
A:Accession: A54645
A:Molecule type: mRNA
A:Residues: 1-562 <HAR>
A:Cross-references: GB:M1518; NID:9190031; PIDN:AAA6011.1; PID:9190032
A>Note: parts of this sequence were confirmed by peptide sequencing
R. Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C.
DNA 6, 461-472, 1987
A:Title: Expression of human uterine tissue-type plasminogen activator in mouse cells
A:Reference number: 160110; MUID:88054470
A:Accession: 160110
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-562 <RES>
A:Cross-references: GB:M1882; NID:9340176; PIDN:AAA6800.1; PID:9340177
R. Fisher, R.; Waller, E.K.; Gross, G.; Thompson, D.; Tizard, R.; Schleuning, W.D.
J. Biol. Chem. 260, 11223-11230, 1985
A:Title: Isolation and characterization of the human tissue-type plasminogen activato
A:Reference number: 155232; MUID:85289338
A:Accession: 155232
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-36 <RE2>
A:Cross-references: GB:M1890; NID:9339837; PIDN:AAA61213.1; PID:9339839
C:Comment: Cleavage by plasmin or trypsin produces two chains held together by a sing
C:Comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond.
C:Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I repea
C:Genetics:
A:Gene: GDB:PLAT
A:Cross-references: GDB:119496; OMIM:173370
A:Map position: 8p12-8p12
A:Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3;
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasmin; serine proteinase
F:1-23/DNA: signal sequence #status predicted <SIG>
F:24-32/DNA: propeptide #status predicted <PRO>
F:33-562/Product: t-plasminogen activator #status experimental <MAT>
F:33-310/Product: t-plasminogen activator chain A #status experimental <ACH>
F:41-78/DNA: EGF homology <EGF>
F:86-119/DNA: EGF homology <EGF>
F:127-208/DNA: kringle homology <KR2>
F:215-262/DNA: kringle homology <KR2>
F:311-562/Product: t-plasminogen activator chain B #status experimental <BCH>
F:311-566/DNA: trypsin homology <TRI>
F:41-71, 69-78, 86-97, 91-108, 110-119, 127-208, 148-190, 179-203, 215-296, 236-278, 267-291, 29
F:152, 483/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:219/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F:310-311/Cleavage site: Arg-11e (plasmin, trypsin) #status experimental
F:357, 406/Active site: His, Asp #status predicted
F:513/Active site: Ser #status experimental

N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C:Species: Torpedo californica (Pacific electric ray)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000
 C:Accession: A47299
 R:Jennings, C.G.; Dyer, S.M.; Burden, S.J.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2895-2899, 1993
 A:Title: Muscle-specific trk-related receptor with a kringle domain defines a distinct C
 A:Reference number: A47299; MUID:93219391
 A:Accession: A47299
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-946 <EN>
 A:Cross-references: GB:LI1311; MID:g290857; PIDN:AAA9285.1; PID:g290858
 A:Experimental source: electric organ
 A:Note: sequence extracted from NCBI backbone (NCBIN:128724, NCSTP:128726)
 C:Superfamily: Torpedo ror-related receptor; immunoglobulin homology; Kringle homology;
 C:Keywords: ATP; glycoprotein; kringle; phosphotransferase; transmembrane protein; tyros
 F:44-103/Domain: immunoglobulin homology <IM1>
 F:137-195/Domain: immunoglobulin homology <IM2>
 F:229-287/Domain: immunoglobulin homology <IM3>
 F:464-542/Domain: kringle homology <KR3>
 F:572-588/Domain: transmembrane #status predicted <TM>
 F:650-940/Domain: protein kinase homology <KIN>
 F:658-666/Region: protein kinase ATP-binding motif
 F:225,340,477,544/Binding site: carbonylrate (Asn) (covalent) #status predicted

Query Match 35.5%; Score 49; DB 1; Length 946;
 Best Local Similarity 57.1%; Pred. No. 54;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 RNPDDVGGPMAYT 14
 ||| |
 Db 514 RNPGESEKPCYT 527

RESULT 44
 T49228
 plasma membrane H+-ATPase-like - Arabidopsis thaliana
 N:Alternate names: protein F27H5.120
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
 C:Accession: T49228
 R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, R
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z25018
 A:Accession: T49228
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-961 <RIE>
 A:Cross-references: EMBL:AL163852; GSPDB:GN00061; ATSP:F27H5.120
 C:Experimental source: cultivar Columbia; BAC clone F27H5
 C:Genetics:
 A:Gene: ATSP:F27H5.120
 A:Map position: 3
 A:Introns: 17/3; 57/3; 90/3; 136/3; 183/1; 241/3; 310/3; 350/3; 390/3; 431/3; 466/3; 515
 C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 F:484-653/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 35.1%; Score 48.5; DB 2; Length 961;
 Best Local Similarity 64.3%; Pred. No. 65;
 Matches 9; Conservative 1; Mismatches 1; Indels 3; Gaps 1;
 QY 3 PDGDV--GGPMAY 13
 |||| |
 Db 469 PDGDVKGEGPWF 482

RESULT 45
 B64318
 hypothetical protein M70145 - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 11-Jan-2000
 C:Accession: B64318

R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
 ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodex,
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
 A:Reference number: A64300; MUID:96337999
 A:Accession: B64318
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-268 <BU>
 A:Cross-references: GB:U67471; GB:L77117; MID:g1590901; PID:g1498914; TIGR:M70145
 C:Genetics:
 A:Map position: REV142991-142185
 C:Superfamily: Methanobacterium conserved hypothetical protein MTH1017

Query Match 34.8%; Score 48; DB 2; Length 268;
 Best Local Similarity 57.1%; Pred. No. 19;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 9 GPWAVTTPRKLYD 22
 ||| |
 Db 13 GPWVTPPMPRES 26

RESULT 46
 T32768
 hypothetical protein F33D11.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
 C:Accession: T32768
 R:Sammons, L.; Wohldmann, P.; Mullen, G.
 submitted to the EMBL Data Library, December 1997
 A:Description: The sequence of C. elegans cosmid F33D11.
 A:Reference number: Z21222
 A:Accession: T32768
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-347 <SAM>
 A:Cross-references: EMBL:AF039720; PIDN:AAB96700.1; GSPDB:GN00019; CESP:F33D11.7
 A:Experimental source: strain Bristol N2; clone F33D11
 C:Genetics:
 A:Gene: CESP:F33D11.7
 A:Map position: 1
 A:Introns: 34/3; 72/3; 104/2; 127/3; 159/3; 187/3; 260/3; 295/3; 324/3
 C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 34.8%; Score 48; DB 2; Length 347;
 Best Local Similarity 42.9%; Pred. No. 25;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 10 PMAYTTPRKLYD 23
 ||| |
 Db 255 PMALKKPKVHDY 268

RESULT 47
 T32881
 hypothetical protein C34B2.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Mar-2000
 C:Accession: T32881
 R:Graves, T.; Sutterer, C.; Hawkins, M.; Wilson, R.
 submitted to the EMBL Data Library, January 1998
 A:Description: The sequence of C. elegans cosmid C34B2.
 A:Reference number: Z21241
 A:Accession: T32881
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-357 <GRA>
 A:Cross-references: EMBL:AF043693; PIDN:AAB97535.1; GSPDB:GN00019; CESP:C34B2.3
 A:Experimental source: strain Bristol N2; clone C34B2
 C:Genetics:

A:Gene: CESP:C34B2.3
A:Map position: 1
A:Introns: 40/3; 79/3; 111/2; 134/3; 166/3; 194/3; 267/3; 302/3; 331/3
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 34.8%; Score 48; DB 2; Length 357;
Best Local Similarity 42.9%; Pred. No. 26;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
OY 10 PMAYTTPRKLYD 23
DB 262 PMAHLKKREVDY 275

RESULT 48
AC3603
2-oxoisovalerate dehydrogenase alpha chain (EC 1.2.4.4) [imported] - Brucella melitensis
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C:Accession: AC3603
R:DeIvecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:1175668
A:Accession: AC3603
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-410 <KRO>
A:Cross-references: GB:AE008918; PIDN:AL53990.1; PID:q17984939; GSPDB:GN00191
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI10748
A:Map position: 11
C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bi
C:Keywords: oxidoreductase

Query Match 34.8%; Score 48; DB 2; Length 410;
Best Local Similarity 42.9%; Pred. No. 30;
Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
OY 2 NPDGDVGPMAYTTNPKRLYD 22
DB 59 NREGAVGPMAGTLTDELKD 79

RESULT 49
F70662
Probable plcC protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: F70662
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987
A:Accession: F70662
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-508 <COL>
A:Cross-references: GB:Z83860; GB:AL123456; NID:g3261681; PIDN:CAB06146.1; PID:q1781256
C:Experimental source: strain H37RV
C:Genetics:
A:Gene: plcC

Query Match 34.8%; Score 48; DB 2; Length 508;
Best Local Similarity 88.9%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 NPDGDVGCP 10

DB 196 NPDGDVGCP 204

RESULT 50
H84099
cell wall-binding protein BH3600 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: H84099
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: H84099
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-461 <STO>
A:Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BA807319.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3600

Query Match 34.1%; Score 47; DB 2; Length 461;
Best Local Similarity 40.0%; Pred. No. 48;
Matches 10; Conservative 4; Mismatches 7; Indels 4; Gaps 1;
OY 1 RNPDGVDGPMAYTTNP---RRLY 21
DB 328 RPA TGDISPFGYRTHPVGTGQRKLH 352

Search completed: November 8, 2002, 09:32:03
Job time : 17 secs

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OM protein - protein search, using sw model

Run on: November 8, 2002, 09:31:21 ; Search time 26 Seconds
(without alignments)
153.034 Million cell updates/sec

Title: US-09-657-431-9

Perfect score: 138

Sequence: 1 RNPBGVGVGPWAYTTPRKLXYD 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

1: SP-archaea:***
2: SP-bacteria:***
3: SP-fungi:***
4: SP-human:***
5: SP-invertebrate:***
6: SP-mammal:***
7: SP-mhc:***
8: SP-organelle:***
9: SP-plant:***
10: SP-rodent:***
11: SP-virus:***
12: SP-vertebrate:***
13: SP-unclassified:***
14: SP-rv:***
15: SP-bacteriophage:***
16: SP-archaeal:***
17: SP-archaeal:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	97.1	334	6	046507 papio hamad
2	134	97.1	810	4	015146 homo sapien
3	128	92.8	812	11	091WJ5 mus musculu
4	122	88.4	812	11	09ROW3 ratu
5	115	88.3	806	6	018783 macropus eu
6	94	68.1	716	11	P70521 ratu
7	90	65.2	709	13	090ZNE brachydanio
8	90	65.2	716	11	091XG8 mus musculu
9	88	63.8	567	4	013208 homo sapien
10	86	62.3	313	13	09PU78 crocodylus
11	86	62.3	704	13	090865 gallu
12	84	60.9	648	4	09HIV4 homo sapien
13	81	58.7	728	6	09BH09 felis silve
14	79	57.2	75	6	09BG09 bos tauru
15	79	57.2	109	6	09NIB8 ovis arie
16	79	57.2	208	4	09BYM0 homo sapien

17	79	57.2	210	4	013494 mus musculu
18	79	57.2	290	4	002935 mus musculu
19	79	57.2	296	4	014519 mus musculu
20	79	57.2	296	4	014519 mus musculu
21	79	57.2	716	13	091691 xenopus lae
22	79	57.2	717	13	P70006 xenopus lae
23	78	56.5	385	5	025101 hermanita m
24	78	56.5	710	13	091402 xenopus lae
25	76	55.1	726	13	090978 gallu
26	72.5	52.3	2869	6	028398 erinaceus e
27	68	49.3	215	13	042341 gallu
28	66.5	48.2	132	4	016609 homo sapien
29	66	47.8	385	13	090WS2 elaphe sp.
30	64.5	46.7	454	6	046506 papio hamad
31	64	46.4	607	13	091001 gallu
32	64	46.4	608	13	09PW7 struthio ca
33	63.5	46.0	113	4	09UR5 homo sapien
34	63	45.7	378	13	090WP0 trachemys s
35	62.5	45.3	105	4	09UR8 homo sapien
36	60	43.5	111	6	077688 oryctolagus
37	59.5	43.1	286	4	09UR7 homo sapien
38	59.5	43.1	113	4	09UR7 homo sapien
39	59.5	43.1	113	4	09UR7 homo sapien
40	59	42.8	420	13	090504 mus musculu
41	56	40.6	263	4	000318 mus musculu
42	56	40.6	263	4	096FE7 mus musculu
43	56	40.6	559	11	091VP2 mus musculu
44	55.5	40.2	113	4	09UR6 mus musculu
45	55	39.9	382	13	090WT4 mus musculu
46	54.5	39.5	117	4	09UGS5 mus musculu
47	54.5	39.5	452	13	090Y90 xenopus lae
48	54.5	39.5	473	11	09BY70 mus musculu
49	54.5	39.5	473	11	09N443 mus musculu
50	54.5	39.5	473	11	092454 ratu

ALIGNMENTS

RESULT 1
ID 046507 PRELIMINARY; PRT: 334 AA.
AC 046507;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Cox L.A., Jett C., Hixson J.E.;
RT "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice Site Mutation is Associated with Deletion of a Single Exon in a Null Allele."
RL Submitted (OCT-1997) to the EMBL/GenBank/DDP databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
DR EMBL: AF029692; AAB97887.1; -
DR HSP: P00747; SHPG.
DR MEROPS: S01.233; -
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00051; Kringle; 1.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.

DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease.
 FT NON_TER
 SQ SEQUENCE 334 AA; 36791 MW; C7DC06E03B965286 CRC64;

Query Match
 Best Local Similarity 97.1%; Score 134; DB 6; Length 334;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNPDDVGPGWATYTNPKRLDY 23
 DB 56 RNPDDVGPGWATYTNPKRLDY 78

RESULT 2
 ID 015146 PRELIMINARY; PRT; 810 AA.

AC 015146;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PLASMINOGEN PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
 RA Mitchell D., Robinson J.H.,
 RT "Expression of recombinant human plasminogen and aglycoplasminogen in
 RT HeLa cells."
 RT F1010101y1s 0:0-0(1991).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.

DR EMBL; M74220; AAA36451.1; -
 DR HSSP; P00747; 2PK4
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR001254; Trypsin.
 DR Pfam; PF00051; kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Signal.
 FT STGNAL
 FT CHAIN 1 19 POTENTIAL.
 FT SEQUENCE 810 AA; 90555 MW; B05C7D4BD0D020B3C CRC64;

Query Match
 Best Local Similarity 97.1%; Score 134; DB 4; Length 810;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 RNPDDVGPGWATYTNPKRLDY 23
 DB 56 RNPDDVGPGWATYTNPKRLDY 78

DB 532 RNPDDVGPGWATYTNPKRLDY 554

RESULT 3

ID 091WJ5 PRELIMINARY; PRT; 812 AA.
 AC 091WJ5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PLASMINOGEN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC014773; AAH14773.1; -
 SQ SEQUENCE 812 AA; 90781 MW; 24173260EA2FPD2 CRC64;

Query Match
 Best Local Similarity 92.8%; Score 128; DB 11; Length 812;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNPDDVGPGWATYTNPKRLDY 23
 DB 532 RNPDDVGPGWATYTNPKRLDY 554

RESULT 4

ID 09ROW3 PRELIMINARY; PRT; 812 AA.
 AC 09ROW3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PLASMINOGEN PROTEIN PRECURSOR (EC 3.4.21.7).
 GN PLASMINOGEN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Bangert K., Johnsen A.H., Thorsen S.;
 RT "Rat plasminogen: cDNA and gene structure."
 RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA MEDLINE=91250378; PubMed=1645711;
 RA Kanalas J.J., Makker S.P.;
 RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
 RT receptor site for plasminogen."
 RT J. Biol. Chem. 266:10825-10829(1991).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC EMBL; AJ242649; CAB46014.1; -
 DR HSSP; P00747; 1PMK.
 DR MEROPS; S01.233; -
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR001400; SOMATOTROPIN.
 DR InterPro; IPR001254; Trypsin.
 DR Pfam; PF00051; kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.


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DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR; 4.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00021; KRINGLE_1; 5.
DR PROSITE: PS50070; KRINGLE_2; 5.
DR PROSITE: PS00338; SOMATOTROPIN_2; UNKNOWN_1.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR HYDROLASE: Serine protease; Signal.
FT SIGNAL 1 19
FT CHAIN 20 812 PLASMINOGEN
FT SEQUENCE 812 AA; 90535 MW; 8C703C51410BC9E CRC64;

Query Match 88.4%; Score 122; DB 11; Length 812;
Best Local Similarity 87.0%; Pred. No. 2e-09;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNPDDVGCPWATYTPRKLYD 23
Db 532 RNPDDVGCPWATYTPRKLYD 554

RESULT 5
ID 018783 PRELIMINARY; PRT; 806 AA.
AC 018783;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PLASMINOGEN.
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=98004511; PubMed=9342350;
RT "Lawn R.M., Schwartz K., Paltay L.;
RT "Convergent evolution of apolipoprotein(a) in primates and hedgehog.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: AF012297; AAB5760.1; -.
DR HSSP: P00747; SHPG.
DR MEROPS: S01.233; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00051; kringle; 5.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR; 4.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00021; KRINGLE_1; 5.
DR PROSITE: PS50070; KRINGLE_2; 5.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR HYDROLASE: Serine protease; Signal.
FT SIGNAL 1 19
FT CHAIN 20 812 PLASMINOGEN
FT SEQUENCE 806 AA; 90981 MW; 95FAA86DC20064D5 CRC64;

Query Match 83.3%; Score 115; DB 6; Length 806;
Best Local Similarity 78.3%; Pred. No. 2.1e-08;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 1 RNPDDVGCPWATYTPRKLYD 23
Db 527 RNPDDVGCPWATYTPRKLYD 549

RESULT 6
ID P70521 PRELIMINARY; PRT; 716 AA.
AC P70521;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MACROPHAGE STIMULATING PROTEIN PRECURSOR.
GN MSP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=97011126; PubMed=8858136;
RA Oshiro K., Iwama A., Matsuno K., Ezaki T., Sakamoto O., Hamaguchi I.,
RA Takasu N., Suda T.;
RT "Molecular cloning of Rat Macrophage-stimulating protein and its
RT involvement in the Male Reproductive System.";
RT Biochem. Biophys. Res. Commun. 227:273-280(1996).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: X95096; CA64473.1; -.
DR HSSP: P00747; IKRN.
DR MEROPS: S01.975; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00051; kringle; 4.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR; 4.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00021; KRINGLE_1; 4.
DR PROSITE: PS50070; KRINGLE_2; 4.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR HYDROLASE: Serine protease; Signal.
FT SIGNAL 1 31
FT CHAIN 20 716 AA; 80733 MW; 06B7DF3EF56D921F CRC64;

Query Match 68.1%; Score 94; DB 11; Length 716;
Best Local Similarity 65.2%; Pred. No. 2.2e-05;
Matches 15; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RNPDDVGCPWATYTPRKLYD 23
Db 429 RNPDDVGCPWATYTPRKLYD 451

RESULT 7
ID Q90ZM6 PRELIMINARY; PRT; 709 AA.
AC Q90ZM6;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR-LIKE 1.
GN HGF1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OX Cypriniformes; Cyprinidae; Danio.
RN NCBI_TaxID=7955;
RP SEQUENCE FROM N.A.
RA Bassett D.I., Wilson S.W.;
RT "Early expression of zebrafish Hepatocyte Growth Factor-Like 1
RL suggests a conserved role in vertebrate neural induction.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF370035; AAK54207.1; -
SQ SEQUENCE 709 AA; 81271 MW; 9907236C5DB73A20 CRC64;

Query Match
Best Local Similarity 65.2%; Score 90; DB 13; Length 709;
Matches 14; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Db 422 RNPDSHGPMWCTMDPRTPEFY 444

RESULT 8
OQ1XG8 PRELIMINARY; PRT; 716 AA.
AC OQ1XG8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DE 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE HEPATOCYTE GROWTH FACTOR-LIKE.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010551; AAH10551.1; -
SQ SEQUENCE 716 AA; 80693 MW; 12474C48A7D4B46D CRC64;

Query Match
Best Local Similarity 65.2%; Score 90; DB 11; Length 716;
Matches 15; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OQ 1 RNPDSGPMWCTMDPRTPEFY 23
Db 429 RNPDSHGPMWCTMDPRTPEFY 451

RESULT 9
OQ13208 PRELIMINARY; PRT; 567 AA.
AC OQ13208;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN HOMOLOG.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20191171; PubMed=10728827;
RA Degen S.J.F., McDowell S.A., Waltz S.E., Gould F., Stuart L.A.,
RA Carritt B.;
RT "Structure of the human DIF1S1A locus: a chromosome 1 locus with 978
RT like protein.";
RL DNA Seq. 8:409-413(1998).
DR EMBL: U28054; AAC63092.1; -
DR HSSP; P00747; 2PK4.
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DR MEROPS; S01.977; -
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Trypsin.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00089; PAN; 1.
DR PRINTS; PR00018; KRINGLE.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS00070; KRINGLE_2; 4.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR Hydrolase; Serine protease.
SQ SEQUENCE 567 AA; 64117 MW; 3FC38B07F1645810 CRC64;

Query Match
Best Local Similarity 63.8%; Score 88; DB 4; Length 567;
Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OQ 1 RNPDSGPMWCTMDPRTPEFY 23
Db 395 QNPDSHGPMWCTMDPRTPEFY 417

RESULT 10
OQ9PU78 PRELIMINARY; PRT; 313 AA.
AC OQ9PU78;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN (FRAGMENT).
OS Crocodylus niloticus (Nile crocodile) (African crocodile).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodyliidae; Crocodylinae; Crocodylus.
OX NCBI_TaxID=8501;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=LIVER;
RA MEDLINE=20022983; PubMed=10555283;
RA Hughes S., Zelus D., Mouchiroud D.;
RT "Warm-blooded isochore structure in Nile crocodile and turtle.";
RL Mol. Biol. Evol. 16:1521-1527(1999).
DR EMBL: A011396; CAB56422.1; -
DR HSSP; P00747; IHPV.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Trypsin.
DR Pfam; PF00051; Kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00018; KRINGLE.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR Hydrolase; Serine protease.
FT NON_TER 1
FT NON_TER 313
SQ SEQUENCE 313 AA; 34793 MW; 8E084704958B5AA2 CRC64;

Query Match
Best Local Similarity 62.3%; Score 86; DB 13; Length 313;
Matches 14; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OQ 1 RNPDSGPMWCTMDPRTPEFY 23
Db 80 RNPDSHGPMWCTMDPRTPEFY 102

RESULT 11
OQ90865
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ID 090865 PRELIMINARY; PRT; 704 AA.
AC 090865:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR-LIKE/MACROPHAGE STIMULATING PROTEIN.
GN HGF1/MSP.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=96029010; PubMed=7554499;
RA Thery C., Sharpe M.J., Bailey S.J., Stern C.D., Gherardi E.;
RT "Expression of HGF/SF, HGF/MSP and c-met suggests new functions
RT during early chick development.";
RL Dev. Genet. 17:90-101(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: X84043; CA58862.1; -.
DR HSSP: P00747; ICEA.
DR MEROPS: S01.977; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00051; Kringle_4.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00473; KR; 4.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00021; KRINGLE_1; 4.
DR PROSITE: PS50070; KRINGLE_2; 4.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR Hydrolase: Serine protease.
SQ SEQUENCE 704 AA; 79341 MW; CAB0DBCC41367C37 CRC64;

Query Match 62.3%; Score 86; DB 13; Length 704;
Best Local Similarity 60.9%; Pred. No. 0.00031;
Matches 14; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 RNPDDVGSPMAYTNPRLXYD 23
DB 416 RNPDDNSHGWCYTMPTPTFDY 438

RESULT 12
O9H1V4 PRELIMINARY; PRT; 648 AA.
AC O9H1V4:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE DJ1182A14.3 (SIMILAR TO MST1 (MACROPHAGE STIMULATING 1 (HEPATOCYTE
DE GROWTH FACTOR-LIKE))).
GN DJ1182A14.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Bird C.;
RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

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DR EMBL: AL137798; CAC17639.1; -.
DR HSSP: P00747; 5HPC.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00051; Kringle_4.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00473; KR; 4.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS50070; KRINGLE_2; 4.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR Hydrolase: Serine protease.
SQ SEQUENCE 648 AA; 72781 MW; 4CE07057350E463 CRC64;

Query Match 60.9%; Score 84; DB 4; Length 648;
Best Local Similarity 76.5%; Pred. No. 0.00056;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNPDDVGSPMAYTNP 17
DB 113 RNPDDPGSPMCHTTP 129

RESULT 13
O9BH09 PRELIMINARY; PRT; 728 AA.
AC O9BH09:
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR HGF.
OS Felis silvestris catus (cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA Kodayashi Y., Nakamura N., Ishizaka T., Masuda K., Ohno K.,
RA Tsujimoto H.;
RT "Molecular cloning of feline hepatocyte growth factor (HGF) cDNA.";
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AB046610; BAB21499.1; -.
DR HSSP: P14210; IBRT.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00051; Kringle_1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR; 4.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00021; KRINGLE_1; UNKNOWN_4.
DR PROSITE: PS50070; KRINGLE_2; 4.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR Hydrolase: Serine protease.
SQ SEQUENCE 728 AA; 83067 MW; 8D7F4A333D1E190A CRC64;

Query Match 58.7%; Score 81; DB 6; Length 728;

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Best Local Similarity 60.9%; Pred. No. 0.0017;
Matches 14; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 RNPDDGVGGPWATYTNPKLYD 23
DB 439 RNPDDAHGFWCTGPNLPWDY 461

RESULT 14

Q9BGN9 PRELIMINARY; PRT; 75 AA.

AC Q9BGN9; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN HEPATOCYTE GROWTH FACTOR (FRAGMENT).

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=UTERUS;
RA Murakami S., Fujiwara C., Miyamoto Y., Takeuchi S., Takahashi S.,
Okuda K.;
RT "Expression and action of hepatocyte growth factor in bovine
endometrial stromal and epithelial cells in vitro."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB056447; BAB35031.1; -
DR HSSP: P14210; 1BHT.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003966; Prothrombin.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR SMART: SM00130; KR; 2.
DR PROSITE: PS00021; KRINGLE_1; UNKNOWN_1.
DR PROSITE: PS50070; KRINGLE_2; 2.
FT NON_TER 1 75
FT NON_TER 1 75
SQ SEQUENCE 75 AA; 8831 MW; 829E9FCC49701B1 CRC64;

Query Match 57.2%; Score 79; DB 6; Length 75;
Best Local Similarity 54.5%; Pred. No. 0.00029;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 RNPDDGVGGPWATYTNPKLYD 22
DB 4 RNPGEGBGFWCTGPNPEVRYE 25

RESULT 15

Q9N1B8 PRELIMINARY; PRT; 109 AA.

AC Q9N1B8; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN HEPATOCYTE GROWTH FACTOR (FRAGMENT).

OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM FROM DAY 1 CYCLIC UTERUS;
RX MEDLINE=20297031; PubMed=10819791;
RA Chen C., Spencer T.E., Bazer F.W.;
RT "Expression of hepatocyte growth factor and its receptor c-met in the
ovine uterus";

RL Biol. Reprod. 62:1844-1850(2000).

DR EMBL: AF213397; AAF25945.1; -
DR HSSP: P14210; 2HG.
DR InterPro: IPR000001; Kringle.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS50070; KRINGLE_2; 1.
FT NON_TER 1 109
FT NON_TER 1 109
SQ SEQUENCE 109 AA; 12501 MW; 1F8BFESDBC0DA5D CRC64;

Query Match 57.2%; Score 79; DB 6; Length 109;
Best Local Similarity 54.5%; Pred. No. 0.00043;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 RNPDDGVGGPWATYTNPKLYD 22
DB 67 RNPGEGBGFWCTGPNPEVRYE 88

RESULT 16

Q9BYM0 PRELIMINARY; PRT; 208 AA.

AC Q9BYM0; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN HEPATOCYTE GROWTH FACTOR (FRAGMENT).

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=91369928; PubMed=1832556;
RA Miyazawa K., Kitamura A., Kitamura N.;
RT "Structural organization and the transcription initiation site of the
human hepatocyte growth factor gene";
RL Biochemistry 30:9170-9176(1991).

DR EMBL: M75971; AAG53459.1; -
DR EMBL: M75967; AAG53459.1; JOINED.
DR EMBL: M75966; AAG53459.1; JOINED.
DR EMBL: M75968; AAG53459.1; JOINED.
DR EMBL: M75969; AAG53459.1; JOINED.
DR HSSP: P14210; 1BHT.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR003966; Prothrombin.
DR Pfam: PF00024; PAN; 1.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR SMART: SM00130; KR; 1.
DR SMART: SM00473; PAN_AP; 1.
DR PROSITE: PS00021; KRINGLE_1; UNKNOWN_1.
DR PROSITE: PS50070; KRINGLE_2; 1.
FT NON_TER 208 208
SQ SEQUENCE 208 AA; 23931 MW; AE9C50DE5A86B37B CRC64;

Query Match 57.2%; Score 79; DB 4; Length 208;
Best Local Similarity 54.5%; Pred. No. 0.00088;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 RNPDDGVGGPWATYTNPKLYD 22
DB 178 RNPGEGBGFWCTGPNPEVRYE 199

RESULT 17
Q13494 PRELIMINARY; PRT; 210 AA.

SQ SEQUENCE 290 AA; 33765 MW; C8A18A6FD63200A CRC64;
 Query Match 57.2%; Score 79; DB 4; Length 290;
 Best Local Similarity 54.5%; Pred. No. 0.0013;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 1 RNPBGVGGPWATYTNPKLYD 22
 ||| : ||| : ||| : ||| :
 DB 178 RNPBGEGGPGWCTSNPEVRYE 199
 ||| : ||| : ||| : ||| :
 RESULT 20
 ID Q14519 PRELIMINARY; PRT; 296 AA.
 AC Q14519;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE COMPETITIVE HGF ANTAGONIST.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Chan A.M.-L., Rubin J.S., Bottaro D.P., Hirschfield D.W., Chedid M.,
 RA Aaronson S.A.;
 RT "Identification of a Competitive HGF Antagonist Encoded by an
 RT Alternative Transcript."
 RL Science 0:0-0(1991)
 DR EMBL; M77227; AAA35980.1; -
 DR HSSP; P14210; 1BHT.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR Pfam; PF00051; Kringle; 2.
 DR Pfam; PF00024; PAN; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00473; PAN_AP; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS0070; KRINGLE_2; 2.
 SQ SEQUENCE 296 AA; 34546 MW; AA5E456B87AE03BE CRC64;
 Query Match 57.2%; Score 79; DB 4; Length 296;
 Best Local Similarity 54.5%; Pred. No. 0.0013;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 1 RNPBGVGGPWATYTNPKLYD 22
 ||| : ||| : ||| : ||| :
 DB 178 RNPBGEGGPGWCTSNPEVRYE 199
 ||| : ||| : ||| : ||| :
 RESULT 21
 ID Q91691 PRELIMINARY; PRT; 716 AA.
 AC Q91691;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GROWTH FACTOR LIVERINE.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ruiz i Altaba A., Thery C.;
 RA Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U57455; AAB52574.1; -
 DR HSSP; P00747; ICEA.

DR MEROPS; S01.UNA; -
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR001254; Trypsin.
 DR Pfam; PF00051; Kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS0070; KRINGLE_2; 4.
 DR PROSITE; PS0240; TRYPsin_DOM; 1.
 KW Hydrolyase; Serine protease.
 SQ SEQUENCE 716 AA; 81971 MW; 508376A0EA398798 CRC64;
 Query Match 57.2%; Score 79; DB 13; Length 716;
 Best Local Similarity 56.5%; Pred. No. 0.0034;
 Matches 13; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 RNPBGVGGPWATYTNPKLYD 23
 ||| : ||| : ||| : ||| :
 DB 426 RNPDRDSHGPGWCTMDNTPFDY 448
 ||| : ||| : ||| : ||| :
 RESULT 22
 ID P70006 PRELIMINARY; PRT; 717 AA.
 AC P70006;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HEPATOCTYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RC MEDLINE=96404125; PubMed=8808403;
 RA Abberger F., Schmidt G., Richter K.;
 RT "The Xenopus homologue of hepatocyte growth factor-like protein is
 RT specifically expressed in the presumptive neural plate during
 RT gastrulation."
 RT Mech. Dev. 54:23-37(1996).
 DR EMBL; Y08734; CAA69989.1; -
 DR HSSP; P00747; ICEA.
 DR MEROPS; S01.977; -
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR001254; Trypsin.
 DR Pfam; PF00051; Kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 3.
 DR PROSITE; PS0070; KRINGLE_2; 4.
 DR PROSITE; PS0240; TRYPsin_DOM; 1.
 KW Hydrolyase; Serine protease; Signal.
 FT SIGNAL 1
 FT CHAIN 29
 FT SEQUENCE 717 AA; 82017 MW; 6F877A432C8CD54 CRC64;
 Query Match 57.2%; Score 79; DB 13; Length 717;
 Best Local Similarity 56.5%; Pred. No. 0.0034;

Matches 13; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 RNPdGVGPMWATTPRKLYD 23
 |||| | ||| | : ||
 DB 427 RNPDRSHGPMWCTTMDPNPFDD 449

RESULT 23

025101
 ID 025101 PRELIMINARY; PRT; 385 AA.
 AC 025101;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE SERINE PROTEINASE.
 GN HSERP1.
 OS Herdmania momus.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyuridae; Herdmania.
 OX NCBI_TaxID=7733;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN-CURVATA:
 RA Arnold J.M., Kennett C., Lavin M.F.;
 RT "Transient expression of a novel serine protease in the ectoderm of
 the ascidian Herdmania momus during development.";
 RL Dev. Genes Evol. 206:455-463(1997).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY.
 CC EMBL: U63517; AAB6650.1; -.
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01.0PA; -.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Trypsin.
 DR Pfam; PF00051; Kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; TRYP-SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYP-SIN_DOM; 1.
 DR PROSITE; PS00134; TRYP-SIN_HIS; 1.
 DR PROSITE; PS00135; TRYP-SIN_SER; 1.
 KW Hydrolyase; Serine protease.
 SQ SEQUENCE 385 AA; 42935 MW; BFBID05D5232E6A0 CRC64;

Query Match 56.5%; Score 78; DB 5; Length 385;
 Best Local Similarity 60.9%; Pred. NO. 0.0024;
 Matches 14; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 1 RNPdGVGPMWATTPRKLYD 23
 |||| | ||| | : ||
 DB 75 RNPdDGMGPMWCTTNEMRMDY 97

RESULT 24

091402
 ID 091402 PRELIMINARY; PRT; 710 AA.
 AC 091402;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HEPATOCYTE GROWTH FACTOR.
 GN HGF.
 OS Xenopus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae.
 OX NCBI_TaxID=8353;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=TAILBUD;
 RX MEDLINE=95267690; PubMed=7748783;
 RA Nakamura H., Tashiro K., Nakamura T., Shiohara K.;
 RT "Molecular cloning of Xenopus HGF cDNA and its expression studies in
 RT Xenopus early embryogenesis.";
 RL Mech. Dev. 49:123-131(1995).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY.

CC EMBL: S77422; AAB34354.2; -.
 DR HSSP; P14210; IBHT.
 DR MEROPS; S01.976; -.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR001254; Trypsin.
 DR Pfam; PF00051; Kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP-SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 3.
 DR PROSITE; PS50070; KRINGLE_2; 4.
 DR PROSITE; PS50240; TRYP-SIN_DOM; 1.
 KW Hydrolyase; Serine protease.
 SQ SEQUENCE 710 AA; 81487 MW; 5FE6480BE31C27FC CRC64;

Query Match 56.5%; Score 78; DB 13; Length 710;
 Best Local Similarity 56.5%; Pred. NO. 0.0047;

Matches 13; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 RNPdGVGPMWATTPRKLYD 23
 |||| | ||| | : ||
 DB 425 RNPdNDAGHGMWCTYDDPFVPMWY 447

RESULT 25

090978
 ID 090978 PRELIMINARY; PRT; 726 AA.
 AC 090978; Q90866;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HEPATOCYTE GROWTH FACTOR / SCATTER FACTOR PRECURSOR.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=EMBRYO;
 RC TISSUE=EMBRYO;
 RX MEDLINE=96029010; PubMed=7554499;
 RA Thery C., Sharpe M.J., Batley S.J., Stern C.D., Gherardi E.;
 RT "Expression of HGF/SF, HGF1/MSF, and C-met suggests new functions
 RT during early chick development.";
 RL Dev. Genet. 17:90-101(1995).
 RN [2]
 RP SEQUENCE OF 1-409 FROM N.A.
 RC STRAIN=WHITE LEHORN, AND RHODE ISLAND RED X LIGHT SUSSEX;
 RC TISSUE=EMBRYO;
 RX MEDLINE=95237013; PubMed=7720585;
 RA Sharpe M.J., Gherardi E.;
 RA Sharpe M.J., Stern C.D., Thery C., Ireland G.W., Aparicio S.,
 RT "A role for HGF/SF in neural induction and its expression in Hensen's
 RT node during gastrulation.";
 RL Development 121:813-824(1995).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY.

DR EMBL: X84045; CAA58864.1; -
 DR EMBL: X80131; CAA56430.1; -
 DR HSSP: P14210; 1BHT.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringleg.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR pfam: PF00051; kringleg_4.
 DR pfam: PF00024; PAN; 1.
 DR pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 4.
 DR SMART: SM00473; PAN_AP; 1.
 DR PROSITE: PS00020; TRYP_SPE; 1.
 DR PROSITE: PS50070; KRINGLE_1; 4.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 KW Alternative splicing; Glycoprotein; Growth factor; Hydrolase; Kringleg;
 KW Serine protease; Serine protease homolog; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 726 HEPATOCYTE GROWTH FACTOR/ SCATTER FACTOR.
 SQ SEQUENCE 726 AA: 82913 MW: 5805F048A5766C38 CRC64;

Query Match 55.1%; Score 76; DB 13; Length 726;
 Best Local Similarity 56.5%; Pred. No. 0.0094;
 Matches 13; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 RNPDDGVGGFWAYTNPRLKLYD 23
 DB 439 RNPDDHFGPCYTDPLIPWDY 461

RESULT 26
 Q28398 PRELIMINARY; PRT; 2869 AA.
 AC 028398.
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE APOLIPOPROTEIN(A) (FRAGMENT).
 OS Erinaceus europaeus (European hedgehog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
 OX NCBI_TaxID=9365;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96025778; PubMed=7592597;
 RA Lawn R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
 RA Byrne C.D., Fong K.J., Meer K., Patchy L.;
 RT "The recurring evolution of lipoprotein(a). Insights from cloning of
 RT hedgehog apolipoprotein(a)."
 RL J. Biol. Chem. 270:24004-24009(1995).
 DR EMBL: U33170; AAC48522.1; -
 DR HSSP: P00747; 1PMK.
 DR InterPro: IPR000001; Kringleg.
 DR Pfam: PF00051; Kringleg_1.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 31.
 DR PROSITE: PS00021; KRINGLE_1; 17.
 DR PROSITE: PS50070; KRINGLE_2; 31.
 KW Lipoprotein.
 FT NON_TER 1 1
 SQ SEQUENCE 2869 AA: 318601 MW: 9527CEF985A4FB2A CRC64;

Query Match 52.5%; Score 72.5; DB 6; Length 2869;
 Best Local Similarity 56.5%; Pred. No. 0.14;
 Matches 13; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
 OY 1 RNPDDGVGGFWAYTNPRLKLYD 23
 DB 439 RNPDDHFGPCYTDPLIPWDY 461

DB 2548 RNPGEV-APWCYTINSARMEY 2569

RESULT 27
 Q42341 PRELIMINARY; PRT; 215 AA.
 AC 042341.
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE HGF ALPHA-CHAIN (FRAGMENT).
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RA Isokawa K., Yahagi N., Honma J., Tanaka M., Murakami K., Yokoyama H.,
 RA Toda Y.;
 RT "The expression of hepatocyte growth factor mRNA is temporally
 RT relevant to cardiac endothelial-mesenchymal transformation."
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D63779; BAA23643.1; -
 DR HSSP: P00747; 1KRN.
 DR InterPro: IPR000001; Kringleg.
 DR Pfam: PF00051; Kringleg_1.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 2.
 DR PROSITE: PS00021; KRINGLE_1; 3.
 DR PROSITE: PS50070; KRINGLE_2; 3.
 FT NON_TER 1 1
 FT NON_TER 215 215
 SQ SEQUENCE 215 AA: 24949 MW: 55B67AB52DAF316 CRC64;

Query Match 49.3%; Score 68; DB 13; Length 215;
 Best Local Similarity 64.7%; Pred. No. 0.037;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 RNPDDGVGGFWAYTNP 17
 DB 198 RNPDDHFGPCYTDPLIPWDY 214

RESULT 28
 Q16609 PRELIMINARY; PRT; 132 AA.
 AC 016609.
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE (APORGC).
 GN APORGC.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=95268939; PubMed=7749817;
 RA Byrne C.D., Schwartz K., Lawn R.M.;
 RT "Loss of a splice donor site at a 'skipped exon' in a gene homologous
 RT to apolipoprotein(a) leads to an mRNA encoding a protein consisting of
 RT a single kringleg domain."
 RL Arterioscler. Thromb. Vasc. Biol. 15:65-70(1995).
 DR EMBL: U19518; AAA85693.1; -
 DR EMBL: U19517; AAA85692.1; -
 DR HSSP: P00747; 1PMK.
 DR InterPro: IPR000001; Kringleg.
 DR Pfam: PF00051; Kringleg_1.
 DR PRINTS: PR00018; KRINGLE.

DR SMART: SM00130; KR: 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 SQ SEQUENCE 132 AA; 14866 MW; 3794AD30A56DBBA CRC64;

Query Match 46.2%; Score 66.5; DB 4; Length 132;
 Best Local Similarity 52.2%; Pred. No. 0.036; Indels 1; Gaps 1;
 Matches 12; Conservative 3; Mismatches 7;

OY 1 RNPBGVGGPMAYTTNPKLYDY 23
 DB 78 RNPDCS-AGPCYCTDPNVRMEY 99

RESULT 29
 O90WS2 PRELIMINARY: PRT: 385 AA.

AC O90WS2: 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PUTATIVE THROMBIN (FRAGMENT).

OS Elaphe sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubridae;
 OC Colubridae; Colubrinae; Elaphe.

NCBI_TaxID=114965;
 RN [1]

SEQUENCE FROM N.A.
 RC TISSUE=LIVER;

RA Hughes S., Laurin M., Mouchiroud D.;
 RT "The phylogenetic position of turtles among saurosidæ remains
 RT contentious with new nuclear data."

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ286868; CAC69543.1; -

FT NON_TER 1
 FT NON_TER 385
 SQ SEQUENCE 385 AA; 43901 MW; BF9E59B93C0C8B7B CRC64;

Query Match 47.8%; Score 66; DB 13; Length 385;
 Best Local Similarity 47.8%; Pred. No. 0.14;
 Matches 11; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 1 RNPBGVGGPMAYTTNPKLYDY 23
 DB 91 RNPDEGVGWCYVDHPNMTYNY 113

RESULT 30
 O46506 PRELIMINARY: PRT: 454 AA.

AC O46506: 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE APOLIPROTEIN A (FRAGMENT).
 GN BABAOA.

OS Papio hamadryas (Hamadryas baboon);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.

NCBI_TaxID=9557;
 RN [1]

SEQUENCE FROM N.A.
 RC COX I.A., Jett C., Hixon J.E.;

RA "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice
 RT Site Mutation is Associated with Deletion of a Single Exon in a Null
 RT Allele."

RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.

DR EMBL: AF029691; AAB97886.1; -

DR HSSP: P00747; 2PK4.
 DR MEROPS: S01.226; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; Kringle; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 2.
 DR PROSITE: PS00020; TRYP-Spc; 1.
 DR PROSITE: PS00021; KRINGLE_1; 2.
 DR PROSITE: PS50070; KRINGLE_2; 2.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Lipoprotein; Serine protease.
 FT NON_TER 1
 SQ SEQUENCE 454 AA; 50041 MW; 974E30744C187B2F CRC64;

Query Match 46.7%; Score 64.5; DB 6; Length 454;
 Best Local Similarity 47.8%; Pred. No. 0.27;
 Matches 11; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

OY 1 RNPBGVGGPMAYTTNPKLYDY 23
 DB 152 RNPDAOT-GPWCFTMDPSVRMEY 173

RESULT 31
 O91001 PRELIMINARY: PRT: 607 AA.

AC O91001: 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE THROMBIN.

OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.

NCBI_TaxID=9031;
 RN [1]

SEQUENCE FROM N.A.
 RC TISSUE=LIVER;

RA Banfield D.K., MacGillivray R.T.;
 RT "Partial characterization of vertebrate prothrombin cDNAs:
 RT amplification and sequence analysis of the B chain of thrombin from
 RT nine different species."

RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
 RN [2]

SEQUENCE FROM N.A.
 RC TISSUE=LIVER;

RA Banfield D.K.;
 RT Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.

DR EMBL: M81391; AAA21619.1; -
 DR HSSP: P00734; 1UVS.

DR MEROPS: S01.217; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00594; gla; 1.

DR Pfam: PF00051; kringle; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR PRINTS: PR00018; KRINGLE.
 DR PRINTS: PR01505; PROTHROMBIN.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00130; KR; 2.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE: PS00021; KRINGLE_1; 2.
 DR PROSITE: PS50070; KRINGLE_2; 2.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR Hydrolase: Serine protease.
 SO SEQUENCE 607 AA; 69110 MW; 002F3606EA36270F CRC64;

Query Match 46.4%; Score 64; DB 13; Length 607;
 Best Local Similarity 58.8%; Pred. NO. 0.44;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 RNPDDVGGPMAYTNP 17
 DB 157 RNPDDVGGPMAYTNP 173

RESULT 32
 ID 09PTW7 PRELIMINARY; PRT; 608 AA.
 AC 09PTW7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROTHROMBIN.
 GN OSPT.
 OS Struthio camelus (Ostrich).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
 OC Struthio.
 OX NCBI_TaxID=8801;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER.
 RX MEDLINE=20579470; PubMed=11137455;
 RA Frost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Ogawa T.;
 RT "Purification and characterization of ostrich prothrombin.";
 RL Int. J. Biochem. Cell Biol. 32:1151-1159(2000)
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY
 DR EMBL: AB028871; BAA89046.1; -.
 DR HSP: P00734; IVS.
 DR MEROPS: S01.217; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00051; kringle; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00001; GLABLOOD.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00130; KR; 2.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE: PS00021; KRINGLE_1; 2.
 DR PROSITE: PS50070; KRINGLE_2; 2.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.

KW Hydrolase: Serine protease.
 SO SEQUENCE 608 AA; 69392 MW; 11B974B9AE54EA2 CRC64;

Query Match 46.4%; Score 64; DB 13; Length 608;
 Best Local Similarity 58.8%; Pred. NO. 0.44;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 RNPDDVGGPMAYTNP 17
 DB 157 RNPDDVGGPMAYTNP 173

RESULT 33
 ID 09URS5 PRELIMINARY; PRT; 113 AA.
 AC 09URS5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE APOLIPOPROTEIN(A) (FRAGMENT).
 GN APOA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21181705; PubMed=11285247;
 RA Ogorekova M., Kraft H.G., Ehrenholm C., Utermann G.;
 RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV
 RT types 6 to 10 domain affect Lp(a) plasma concentrations and have
 RL Hum. Mol. Genet. 10:815-824(2001).
 DR EMBL: AF158663; AAF03680.1; -.
 DR EMBL: AF158663; AAF03680.1; JOINED.
 DR HSP: P00747; 1PMK.
 DR InterPro: IPR000001; Kringle.
 DR Pfam: PF00051; kringle; 1.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 KW Lipoprotein.
 FT NON_TER 1 1
 FT NON_TER 113 113
 SO SEQUENCE 113 AA; 12685 MW; F3D65681D9B5253A CRC64;

Query Match 46.0%; Score 63.5; DB 4; Length 113;
 Best Local Similarity 47.8%; Pred. NO. 0.083;
 Matches 11; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

OY 1 RNPDDVGGPMAYTNPRTKLYD 23
 DB 61 RNPDDVGGPMAYTNPRTKLYD 82

RESULT 34
 ID 09OWP0 PRELIMINARY; PRT; 378 AA.
 AC 09OWP0;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE THROMBIN (FRAGMENT).
 GN THROMBIN.
 OS Trachemys scripta elegans.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.
 OX NCBI_TaxID=31138;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER.
 RA Hughes S., Laurin M., Gouy M., Mouchiroud D.;

"The phylogenetic position of turtles among sauropsidae remains contentious with new nuclear data."
RT Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ286869; CAC69549.1; -
FT NON_TER 1
FT SEQUENCE 378 AA; 42817 MW; 62F09CCTA81059DC CRC64;
SQ

Query Match 45.7%; Score 63; DB 13; Length 378;
Best Local Similarity 43.5%; Pred. No. 0.37;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY 1 RNPDDGVPWATYTNPKLYDY 23
DB 88 RNPDDDEGVCYVDHPNTTFEX 110

RESULT 35

OQ9IR8 PRELIMINARY; PRT; 105 AA.

AC OQ9IR8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DR APOLIPROTEIN(A) (FRAGMENT).
GN APOA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21181705; PubMed=11285247;
RX Ogorekova M., Kraft H.G., Ehnholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringle IV
RT types 6 to 10 domain affect lip(a) plasma concentrations and have
RT different patterns in Africans and Caucasians.";
RL Hum. Mol. Genet. 10:815-824(2001).
DR EMBL: AF158656; AAF03677.1; -
DR EMBL: AF158655; AAF03677.1; JOINED.
DR HSP; P00747; 2PK4.
DR InterPro: IPR000001; Kringle.
DR Pfam: PF00051; Kringle; 1.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS50070; KRINGLE_2; 1.
KW Lipoprotein.
FT NON_TER 1
FT SEQUENCE 105 AA; 11882 MW; 6ECB6C02CD30EFA2 CRC64;
SQ

Query Match 45.3%; Score 62.5; DB 4; Length 105;
Best Local Similarity 43.5%; Pred. No. 0.11;
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

OY 1 RNPDDGVPWATYTNPKLYDY 23
DB 61 RNPDAET-SPWCYTMPDNYRWEY 82

RESULT 36

O77688 PRELIMINARY; PRT; 111 AA.

AC O77688;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DR PROTHROMBIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=LIVER;
RX MEDLINE=99003227; PubMed=9766880;

RA Lee T.H., Rhim T., Kim S.S.;
RT "Prothrombin kringle-2 domain has a growth inhibitory activity against
RT basic fibroblast growth factor-stimulated capillary endothelial
RT cells.";
RL J. Biol. Chem. 273:28805-28812(1998).
DR EMBL: AF080065; AAC71006.1; -
DR HSP; P00735; 1A0H.
DR InterPro: IPR000001; Kringle.
DR Pfam: PF00051; Kringle; 1.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS50070; KRINGLE_2; 1.
FT NON_TER 1
FT SEQUENCE 111 AA; 12168 MW; CB86624D8D7F9DE9 CRC64;
SQ

Query Match 43.5%; Score 60; DB 6; Length 111;
Best Local Similarity 43.5%; Pred. No. 0.27;
Matches 10; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

OY 1 RNPDDGVPWATYTNPKLYDY 23
DB 65 RNPDDGEMARYVAGRPSSEY 87

RESULT 37

ID O13209 PRELIMINARY; PRT; 286 AA.
AC O13209;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DR HEPATOCTE GROWTH FACTOR-LIKE PROTEIN HOMOLOG (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=LIVER.
RC MEDLINE=20191171; PubMed=10728827;
RX Degen S.J.F., McDowell S.A., Waltz S.E., Gould F., Stuart L.A.,
RA Carritt B.;
RT "Structure of the human DFI51A locus: a chromosome 1 locus with 97%
RT identity to the chromosome 3 gene coding for hepatocyte growth factor-
RT like protein.";
RL DNA Seq. 8:409-413(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: U28055; AAC35412.1; -
DR HSP; P00747; SHPG.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00130; KR; 1.
DR SMART: SM00020; TRYP-SPC; 1.
DR PROSITE: PS50070; KRINGLE_2; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
KW Hydrolyase; Serine protease.
FT NON_TER 1
FT SEQUENCE 286 AA; 31986 MW; 43489B747C8D3F90 CRC64;
SQ

Query Match 43.5%; Score 60; DB 4; Length 286;
Best Local Similarity 60.0%; Pred. No. 0.75;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 9 GPMAYTTPRKLYDY 23
 ||| || :|| :||
 Db 3 GPMCTMDPRTPFY 17

RESULT 38

ID Q9UKJ7 PRELIMINARY; PRT; 60 AA.

AC Q9UKJ7;

DT 01-MAY-2000 (TREMBLREL. 13, Created)

DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)

DE APOLIPOPROTEIN(A) (FRAGMENT).

GN APOA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-21181705; PubMed-11285247;

RT "Single nucleotide polymorphisms in exons of the apo(a) kringle IV

RT types 6 to 10 domain affect Lp(a) plasma concentrations and have

RT different patterns in Africans and Caucasians."

RL Hum. Mol. Genet. 10:815-824(2001).

DR EMBL; AF158657; AAF03676.1; -

DR HSSP; P00747; 1KR.

DR InterPro; IPR000001; Kringle.

DR Pfam; PF00051; Kringle; 1.

DR SMART; SM00130; KR; 1.

DR PROSITE; PS00021; KRINGLE_1; 1.

DR PROSITE; PS50070; KRINGLE_2; 1.

KW Lipoprotein.

FT NON_TER 1 1

FT NON_TER 60 60

SQ SEQUENCE 60 AA; 6799 MW; 5719AA26B3E0FF1D CRC64;

Query Match 43.1%; Score 59.5; DB 4; Length 60;
 Best Local Similarity 43.5%; Pred. No. 0.16;
 Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

RESULT 39

ID Q9UIR7 PRELIMINARY; PRT; 113 AA.

AC Q9UIR7;

DT 01-MAY-2000 (TREMBLREL. 13, Created)

DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)

DE APOLIPOPROTEIN(A) (FRAGMENT).

GN APOA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-21181705; PubMed-11285247;

RT "Single nucleotide polymorphisms in exons of the apo(a) kringle IV

RT types 6 to 10 domain affect Lp(a) plasma concentrations and have

DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 KW Lipoprotein.
 FT NON_TER 1 1
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12815 MW; 4F80ADF8708548CB CRC64;

Query Match 43.1%; Score 59.5; DB 4; Length 113;
 Best Local Similarity 43.5%; Pred. No. 0.32;
 Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

OY 1 RNPDGVGPMAYTTPRKLYDY 23

Db 61 RNPDAEI-RPMCTMDPSVMEY 82

RESULT 40

ID Q90504 PRELIMINARY; PRT; 420 AA.

AC Q90504;

DT 01-NOV-1996 (TREMBLREL. 01, Created)

DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)

DE THROMBIN.

OS Eptaretus stoutii (Pacific hagfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;

OC Myxiniidae; Eptaretinae; Eptaretus.

OC NCBI_TaxID=7765;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-92212913; PubMed-1557383;

RT "Partial characterization of vertebrate prothrombin cDNAs:

RT amplification and sequence analysis of the B chain of thrombin from

RT nine different species."

RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE-94223694; PubMed-7513365;

RT "Evolution of prothrombin: isolation and characterization of the cDNAs

RT encoding chicken and hagfish prothrombin."

RL J. Mol. Evol. 38:177-187(1994).

RN [3]

RP SEQUENCE FROM N.A.

RA MEDLINE-94223694; PubMed-7513365;

RT "Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases

RT -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

TRYPsin FAMILY.

CC EMBL; M81393; AAA21620.1; -
 CC HSSP; P00734; 1UVS.
 DR MEROPS; S01.217; -
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Trypsin.
 DR Pfam; PF00051; Kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 KW Hydrolyase; Serine protease.

SQ SEQUENCE 420 AA; 47888 MW; 64522AA21A57B67A CRC64;

Query Match 42.8%; Score 59; DB 13; Length 420;
 Best Local Similarity 71.4%; Pred. No. 1.6;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 RNPDDGVGPMAYT 14
 ||||| | | | |
 DB 64 RNPDDSEGVWCYT 77

RESULT 41

000318 PRELIMINARY; PRT; 263 AA.
 AC 000318;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DE WUGSC:DJ515N1.2, Last annotation update)
 DE WUGSC:DJ515N1.2, PROTEIN.
 GN WUGSC:DJ515N1.2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Du Z., Scheet P., Harper M.,
 RT "The sequence of H. sapiens RP3-515N1."
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC002073; AAB54054.1;
 DR HSSP: P00749; IKDU.
 DR InterPro: IPR000001; Kringle.
 DR Pfam: PF00051; Kringle; 1.
 DR PRINTS: PR00018; KRINGLE; FALSE_NEG.
 DR SMART: SM00130; KR; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 DR SEQUENCE 263 AA; 28248 MW; 197C3EEB854A242 CRC64;
 SQ
 Query Match 40.6%; Score 56; DB 4; Length 263;
 Best Local Similarity 60.0%; Pred. No. 2.6;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

RESULT 42

096E7 PRELIMINARY; PRT; 263 AA.
 AC 096E7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE UNKNOWN (PROTEIN FOR MGC:17330).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN, AND ANAPLASTIC OLIGODENDROGLIOMA WITH 1P/19Q LOSS;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC011049; AAH11049.1;
 DR SEQUENCE 263 AA; 28234 MW; 197C3EEB88FA242 CRC64;
 SQ

Query Match 40.6%; Score 56; DB 4; Length 263;
 Best Local Similarity 60.0%; Pred. No. 2.6;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 RNPDDGVGPMAYT 15
 ||||| | | | |
 DB 71 RNPDDPRGPMCYVS 85

RESULT 43

091VP2 PRELIMINARY; PRT; 559 AA.
 AC 091VP2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SIMILAR TO PLASMINOGEN ACTIVATOR, TISSUE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BREAST TUMOR;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC011256; AAH11256.1;
 DR SEQUENCE 559 AA; 63122 MW; 8CCE2BDB9451AD9 CRC64;
 SQ

Query Match 40.6%; Score 56; DB 11; Length 559;
 Best Local Similarity 50.0%; Pred. No. 5.9;
 Matches 12; Conservative 3; Mismatches 7; Indels 2; Gaps 2;

OY 1 RNPDDGVGPMAYTTPKLT-YDY 23
 ||||| | | | |
 DB 266 RNPDD-ARPMCHWKDKRLTMEY 288

RESULT 44

09UR6 PRELIMINARY; PRT; 113 AA.
 AC 09UR6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE APOLOPROTEIN(A) (FRAGMENT).
 GN APOA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2181705; PubMed=11285247;
 RA Ogorekova M., Kraft H.G., Ehnholm C., Utermann G.;
 RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV
 types 6 to 10 domain affect lip(a) plasma concentrations and have
 different patterns in Africans and Caucasians."
 RL Hum. Mol. Genet. 10:815-824 (2001).
 DR EMBL: AF158661; AAF03679.1;
 DR EMBL: AF158660; AAF03679.1; JOINED.
 DR HSSP: P00747; 2PK4.
 DR InterPro: IPR000001; Kringle.
 DR Pfam: PF00051; Kringle; 1.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 DR Lipoprotein.
 FT NON_TER 1 1
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12697 MW; 51D4461D9C66312E CRC64;
 SO

Query Match 40.2%; Score 55.5; DB 4; Length 113;
 Best Local Similarity 47.8%; Pred. No. 1.2;

Matches 11; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 1 RNPDDGVGGPMAYTTPKRLYDY 23
 |||||
 Db 61 RNPDSG-KOPWCYTTDPCYRWEY 82

RESULT 45

ID 090WT4 PRELIMINARY; PRT; 382 AA.
 AC 090WT4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 GN THROMBIN.
 OS Crocodylus niloticus (Nile crocodile) (African crocodile).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodyliae; Crocodylinae; Crocodylus.
 NCBI_TaxID=8501;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Hughes S., Laurin M., Gouy M., Mouchiroud D.;
 RT "The phylogenetic position of turtles among saurropsidae remains
 RT controversial with new nuclear data."
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ286873; CAC69536.1;
 FT NON_TER 1
 FT 382
 SQ SEQUENCE 382 AA; 43282 MW; FE8E60239D8CBEBC CRC64;

Query Match 39.9%; Score 55; DB 13; Length 382;
 Best Local Similarity 43.5%; Pred. No. 5.5;
 Matches 10; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 RNPDDGVGGPMAYTTPKRLYDY 23
 |||||
 Db 89 RNPDDGEGWCVTGGEPPDFEX 111

RESULT 46

ID 09UGS5 PRELIMINARY; PRT; 117 AA.
 AC 09UGS5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BK747E2.4 (NOVEL KRINGLE AND CUB DOMAIN PROTEIN) (FRAGMENT).
 GN BK57G9.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ho S.;
 RT Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AL021393; CAB62959.1;
 DR HSSP; P00747; 1PML.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; Kringle.1.
 DR PRINTS; PR00018; Kringle.1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 FT NON_TER 1
 FT 117
 SQ SEQUENCE 117 AA; 12673 MW; F4270BBA1D03EDCE CRC64;

Query Match 39.5%; Score 54.5; DB 4; Length 117;
 Best Local Similarity 76.9%; Pred. No. 1.8;
 Matches 10; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 RNPDDGVGGPMAY 13
 |||||
 Db 87 RNPDDGV-SPWCY 98

RESULT 47

ID 090Y90 PRELIMINARY; PRT; 452 AA.
 AC 090Y90;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 GN KREMEN.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2167372; PubMed=11267660;
 RA Nakamura T., Aoki S., Kitajima K., Funakoshi H., Takahashi T.,
 RA Matsumoto K., Nakamura T.;
 RT "Molecular cloning and characterization of Kremen, a novel kringle-
 RT containing transmembrane protein."
 RL Biochim. Biophys. Acta 1518:63-72(2001).
 DR EMBL; AB070851; BAB64294.1;
 SQ SEQUENCE 452 AA; 50188 MW; ED24BCD1A94564E2 CRC64;

Query Match 39.5%; Score 54.5; DB 13; Length 452;
 Best Local Similarity 76.9%; Pred. No. 7.8;
 Matches 10; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 RNPDDGVGGPMAY 13
 |||||
 Db 83 RNPDDGV-SPWCY 94

RESULT 48

ID 09BY70 PRELIMINARY; PRT; 473 AA.
 AC 09BY70;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE KRINGLE-CONTAINING TRANSMEMBRANE PROTEIN.
 GN KREMEN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21167372; PubMed=11267660;
 RA Nakamura T., Aoki S., Kitajima K., Funakoshi H., Takahashi T.,
 RA Matsumoto K., Nakamura T.;
 RT "Molecular cloning and characterization of Kremen, a novel kringle-
 RT containing transmembrane protein."
 RL Biochim. Biophys. Acta 1518:63-72(2001).
 CC -1 SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL; AB059618; BAB40969.1;
 DR HSSP; P00747; 1PML.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF01822; WSC; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00321; WSC; 1.

DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 KW Transmembrane.
 SQ SEQUENCE 473 AA; 51744 MW; F6D30DDE708C186B CRC64;

Query Match 39.5%; Score 54.5; DB 4; Length 473;
 Best Local Similarity 76.9%; Pred. No. 8.2;
 Matches 10; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 1 RNPDGVDYGGPWAY 13
 ||||| |||
 DB 85 RNPDGDV-SPWCY 96

RESULT 49

O99N43 PRELIMINARY; PRT; 473 AA.

AC O99N43;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE KRINGLE-CONTAINING TRANSMEMBRANE PROTEIN.
 GN KREMEN OR KREMEN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-21167372; PubMed-11267660;
 RA Nakamura T., Aoki S., Kitajima K., Funakoshi H., Takahashi T.,
 RA Matsumoto K., Nakamura T.;
 RT "Molecular cloning and characterization of Kremen, a novel kringle-
 containing transmembrane protein."
 RL Biochim. Biophys. Acta 1518:63-72(2001).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.

DR EMBL; AB059617; BAB40968.1; -.
 DR HSSP; P00747; ICEA.
 DR MCD; MGI:1933988; Kremen.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR002889; WSC.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00051; Kringle; 1.
 DR Pfam; PF01822; WSC; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00321; WSC; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 KW Transmembrane.
 SQ SEQUENCE 473 AA; 51716 MW; 586827788B3FDD1 CRC64;

Query Match 39.5%; Score 54.5; DB 11; Length 473;
 Best Local Similarity 76.9%; Pred. No. 8.2;
 Matches 10; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 1 RNPDGVDYGGPWAY 13
 ||||| |||
 DB 85 RNPDGDV-SPWCY 96

RESULT 50

O924S4 PRELIMINARY; PRT; 473 AA.

AC O924S4;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE KRINGLE-CONTAINING TRANSMEMBRANE PROTEIN.

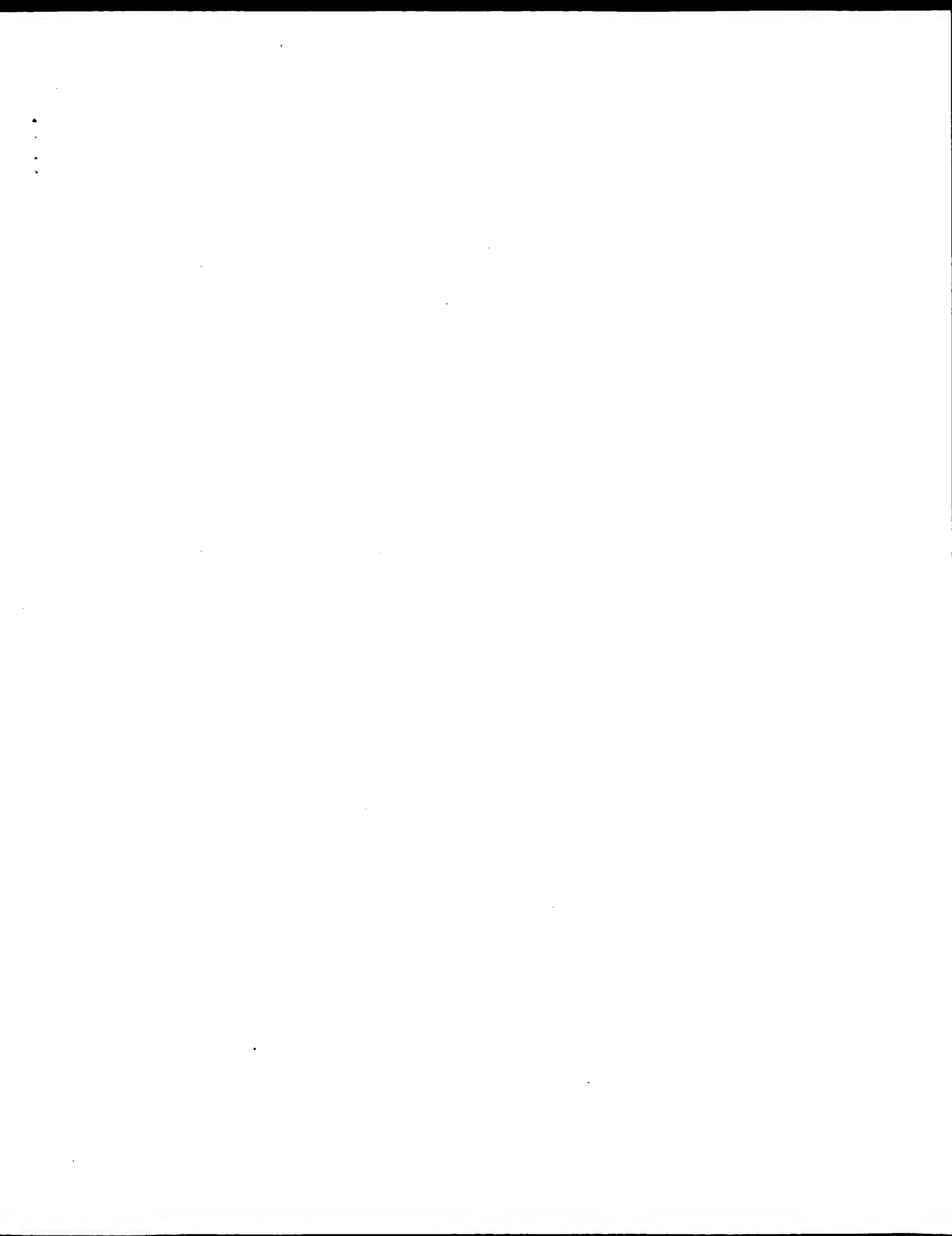
GN KREMEN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-21167372; PubMed-11267660;
 RA Nakamura T., Aoki S., Kitajima K., Takahashi T., Matsumoto K.,
 RA Nakamura T.;
 RT "Molecular cloning and characterization of Kremen, a novel kringle-
 containing transmembrane protein."
 RL Biochim. Biophys. Acta 1518:63-72(2001).
 DR EMBL; AB065090; BAB62003.1; -.
 KW Transmembrane.
 SQ SEQUENCE 473 AA; 51869 MW; 9B510857DF856F08 CRC64;

Query Match 39.5%; Score 54.5; DB 11; Length 473;
 Best Local Similarity 76.9%; Pred. No. 8.2;
 Matches 10; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 1 RNPDGVDYGGPWAY 13
 ||||| |||
 DB 85 RNPDGDV-SPWCY 96

Search completed: November 8, 2002, 09:33:33
 Job time : 29 secs



GenCore version 5.1.3
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OK protein - protein search, using sw model

Run on: November 8, 2002, 09:31:20 ; Search time 10 Seconds
(without alignments)
89.055 Million cell updates/sec

Title: US-09-657-431-9

Perfect score: 138
Sequence: 1 RNPDGVDGGMATTTNPKRLDY 23

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: SwissProt_40:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134	97.1	810	1 PLMN_HUMAN	P00747 homo sapien
2	130	94.2	810	1 PLMN_MACMU	P12545 macaca mula
3	128	92.8	812	1 PLMN_MOUSE	P20918 mus musculu
4	124	89.9	343	1 PLMN_SHEEP	P81286 ovins aries
5	120	87.0	810	1 PLMN_ERIEU	Q29485 erinaceus e
6	117	84.8	4548	1 APOA_HUMAN	P08819 homo sapien
7	114	82.6	338	1 PLMN_HORSE	P80010 equus cabal
8	113	81.9	790	1 PLMN_PIG	P06867 sus scrofa
9	111	80.4	812	1 PLMN_BOVIN	P06868 bos taurus
10	110	79.7	333	1 PLMN_CANFA	P80009 canis famill
11	92	66.7	711	1 HGF_HUMAN	P26927 homo sapien
12	90	65.2	716	1 HGF_MOUSE	P26928 mus musculu
13	82	59.4	728	1 HGF_RAT	P17945 ratuus norv
14	81	58.7	728	1 HGF_HUMAN	P14210 homo sapien
15	80	58.7	728	1 HGF_MOUSE	Q08048 mus musculu
16	80	58.0	625	1 THRB_BOVIN	P00735 bos taurus
17	77	55.8	169	1 PLMN_RAT	Q01177 ratuus norv
18	73	52.9	325	1 PLMN_PPTMA	P33574 petromyzon
19	73	52.9	617	1 THRB_RAT	P18292 ratuus norv
20	71	51.4	618	1 THRB_MOUSE	P19221 mus musculu
21	71	51.4	622	1 THRB_HUMAN	P00734 homo sapien
22	65.5	47.5	1420	1 APOA_MACMU	P14417 macaca mula
23	60	43.5	435	1 YE90_MYCTU	P71771 mycobacteri
24	59	42.8	943	1 ROR2_HUMAN	Q01974 homo sapien
25	59	42.8	944	1 ROR2_MOUSE	Q02138 mus musculu
26	56	40.6	539	1 TPA_MOUSE	P11214 mus musculu
27	56	40.6	700	1 PHLN_BURPS	P19637 ratuus norv
28	52.5	38.0	700	1 PHLN_MOUSE	Q0958 burholderi
29	52	37.7	194	1 TPA_HUMAN	P00750 homo sapien
30	51	37.0	194	1 Y4HQ_RHISN	P50361 rhizobium s
31	51	37.0	198	1 EST1_SCHGA	P81429 schizaphis
32	51	37.0	532	1 ESTE_MZTPE	P35501 myzus persi
33	51	37.0	564	1 ESTE_MZTPE	P35502 myzus persi

34	51	37.0	566	1 TPA_BOVIN	Q28198 bos taurus
35	50.5	36.6	394	1 URTG_DESRO	P49150 desmodus ro
36	49	35.5	615	1 PMA7_HUMAN	P00748 homo sapien
37	48.5	35.1	961	1 PMA7_ARATH	Q91Y32 arabidopsis
38	48	34.8	268	1 Y145_MCTUA	Q57609 methanococ
39	48	34.8	517	1 PHLC_MYCTU	P95245 mycobacteri
40	47	34.1	520	1 GAG_SIVAI	P27192 simian immu
41	46.5	33.7	129	1 TRD5_ECOLI	P27192 escherichia
42	46	33.3	347	1 POR2_HUMAN	P45880 homo sapien
43	46	33.3	519	1 GAG_SIVAT	P05892 simian immu
44	46	33.3	521	1 GAG_SIVAG	P27878 simian immu
45	46	33.3	603	1 FA12_CAVPO	Q04562 cavia porce
46	45.5	33.0	373	1 YHX6_YEAST	P38866 saccharomyc
47	45.5	33.0	514	1 OASL_HUMAN	Q15646 homo sapien
48	45.5	33.0	607	1 PPO_VITVI	P43311 vitis vinif
49	45	33.0	761	1 NETR_MOUSE	Q08762 mus musculu
50	45	32.6	427	1 FOLD_YEAST	Q12676 saccharomyc

ALIGNMENTS

RESULT 1
PLMN_HUMAN STANDARD: PRT: 810 AA.

AC P00747;
21-JUN-1986 (Rel. 01, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Plasmidogen precursor (EC 3.4.21.7) [Contains: Angiostatin].

GN PLC.

OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RN MEDLINE=90202879; PubMed=2318848;

RA Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;

RT "Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system.";

RT J. Biol. Chem. 265:6104-6111(1990).

RN [2]

RN MEDLINE=87162490; PubMed=3030813;

RA Forsgren M., Raden B., Israelsson M., Larsson K., Heden L.O.;

RT "Molecular cloning and characterization of a full-length cDNA clone for human plasminogen.";

RT FEBS Lett. 213:254-260(1987).

RN [3]

RN MEDLINE=75093329; PubMed=122932;

RA Wiman B., Wallen P.;

RT "Structural relationship between 'glutamic acid' and 'lysine' forms of human plasminogen and their interaction with the NH2-terminal activation peptide as studied by affinity chromatography.";

RT Eur. J. Biochem. 50:489-494(1975).

RN [6]

RN MEDLINE=95-580; 581-626; 657-700 AND 732-810.

RA Sottrup-Jensen L., Claeys H., Zafael M., Petersen T.E., Magnusson S.;

RT (In) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);

RT Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,

- RL Raven Press, New York (1978).
 RN [17]
 RP SEQUENCE OF 483-604.
 RX MEDLINE=76043692; PubMed=126863;
 RA Wiman B., Wallen P.;
 RT "Amino-acid sequence of the cyanogen-bromide fragment from human
 RL Eur. J. Biochem. 58:539-547(1975).
 RN [8]
 RP SEQUENCE OF 581-810.
 RX MEDLINE=77225245; PubMed=142009;
 RA Wiman B.;
 RT "Primary structure of the B-chain of human plasmin.";
 RL Eur. J. Biochem. 76:129-137(1977).
 RN [9]
 RP ACTIVE SITE.
 RX MEDLINE=73149248; PubMed=4694729;
 RA Robbins K.C., Bernabe P., Arzadon L., Summaria L.;
 RT "The primary structure of human plasminogen. II. The histidine loop
 RL of human plasmin: light (B) chain active center histidine sequence.";
 RN J. Biol. Chem. 248:1631-1633(1973).
 RN [10]
 RP ACTIVE SITE.
 RX MEDLINE=69234739; PubMed=4240117;
 RA Groskopf W.R., Summaria L., Robbins K.C.;
 RT "Studies on the active center of human plasmin. Partial amino acid
 RL sequence of a peptide containing the active center serine residue.";
 RN J. Biol. Chem. 244:3590-3597(1969).
 RN [11]
 RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
 RX MEDLINE=82213905; PubMed=6919539;
 RA Trexler M., Valli Z., Paltay L.;
 RT "Structure of the omega-aminocarboxylic acid-binding sites of human
 RL plasminogen. Arginine 70 and aspartic acid 56 are essential for
 binding of ligand by kringles 4.";
 RN J. Biol. Chem. 257:7401-7406(1982).
 RN [12]
 RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
 RX MEDLINE=85054794; PubMed=6094526;
 RA Valli Z., Paltay L.;
 RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
 RL are essential for fibrin affinity of the kringles 1 domain.";
 RN J. Biol. Chem. 259:13690-13694(1984).
 RN [13]
 RP PHOSPHORYLATION SITE SER-597.
 RX MEDLINE=97345939; PubMed=9201958;
 RA Wang H., Protok M., Bretthauer R.K., Castellino F.J.;
 RT "Serine-578 is a major phosphorylation locus in human plasma
 RL plasminogen.";
 RN Biochemistry 36:8100-8106(1997).
 RN [14]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Merli T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
 RT Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
 RL "The N- and O-linked carbohydrate chains of human, bovine and porcine
 plasminogen. Species specificity in relation to sialylation and
 RT N-glycosylation patterns.";
 RN Eur. J. Biochem. 173:57-63(1988).
 RN [15]
 RP CARBOHYDRATE-LINKAGE SITE 268.
 RX MEDLINE=97207306; PubMed=9054441;
 RA Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,
 RT Pizzo S.V.;
 RL "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
 human plasminogen 2.";
 RN J. Biol. Chem. 272:7408-7411(1997).
 RN [16]
 RP CHARACTERIZATION OF ANGIOSTATIN AND PARTIAL SEQUENCE.
 RX MEDLINE=95042728; PubMed=7525077;
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 RL Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
 suppression of metastases by a Lewis lung carcinoma.";
 RL Cell 79:315-328(1994).
 RN [17]
 RP CHARACTERIZATION OF ANGIOSTATIN.
 RX MEDLINE=97238710; PubMed=9102221;
 RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
 RL Lapcevic R., Nacy C.A.;
 RT "A recombinant human angiostatin protein inhibits experimental primary
 RL and metastatic cancer.";
 RN Cancer Res. 57:1329-1334(1997).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
 RX MEDLINE=92031502; PubMed=1657148;
 RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
 RT "Crystal and molecular structure of human plasminogen kringles 4
 RL refined at 1.9-A resolution.";
 RN Biochemistry 30:10576-10588(1991).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
 RX MEDLINE=92031503; PubMed=1657149;
 RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
 RT "The refined structure of the epsilon-aminocaproic acid complex of
 RL human plasminogen kringles 4.";
 RN Biochemistry 30:10589-10594(1991).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
 RX Spec B., Yamano A., Whitlow M., Teeter M.M.;
 RT Submitted (JUN-1995) to the PDB data bank.
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
 RX MEDLINE=96180681; PubMed=8611560;
 RA Mathews I.J., Vanderhoff-Hanover P., Castellino F.J., Tulinsky A.;
 RT "Crystal structures of the recombinant kringles 1 domain of human
 RL plasminogen in complexes with the ligands epsilon-aminocaproic acid
 and trans-4-(aminomethyl)cyclohexane-1-carboxylic acid.";
 RN Biochemistry 35:2567-2576(1996).
 RN [22]
 RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
 RX MEDLINE=98198034; PubMed=9521645;
 RA Chang Y., Mochalkin I., McConce S.G., Cheng B., Tulinsky A.,
 RT Castellino F.J.;
 RL "Structure and ligand binding determinants of the recombinant kringles
 5 domain of human plasminogen.";
 RN Biochemistry 37:3258-3271(1998).
 RN [23]
 RP STRUCTURE BY NMR OF 96-184.
 RX MEDLINE=94237157; PubMed=8181475;
 RA Rejzante M.R., Llinas M.;
 RT "1H-NMR assignments and secondary structure of human plasminogen
 RL kringles 1.";
 RN Eur. J. Biochem. 221:927-937(1994).
 RN [24]
 RP STRUCTURE BY NMR OF 96-184.
 RX MEDLINE=94237158; PubMed=8181476;
 RA Rejzante M.R., Llinas M.;
 RT "Solution structure of the epsilon-aminohexanoic acid complex of
 RL human plasminogen kringles 1.";
 RN Eur. J. Biochem. 221:939-949(1994).
 RN [25]
 RP STRUCTURE BY NMR OF 183-354.
 RX MEDLINE=96194156; PubMed=8652577;
 RA Soehnlel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
 RL Rickli E.E.;
 RT "Recombinant gene expression and 1H NMR characteristics of the
 RL kringles (2 + 3) supermodule: spectroscopic/functional individuality
 of plasminogen kringles domains.";
 RN Biochemistry 35:2357-2364(1996).
 RN [26]
 RP STRUCTURE BY NMR OF 374-461.
 RX MEDLINE=90219023; PubMed=2157850;
 RA Atkinson R.A., Williams R.J.P.;
 RT "Solution structure of the kringles 4 domain from human plasminogen by
 1H nuclear magnetic resonance spectroscopy and distance geometry.";

RL J. Mol. Biol. 212:541-552(1990).
RN [27]
RP VARIANTS PHE-374 AND THR-620.
RX MEDLINE=91095410; PubMed=1986355;
RA Ichinose A., Espling E.S., Takamatsu J., Saito H., Shimoyozu K.,
Query Match 97.1%; Score 134; DB 1; Length 810;
Best Local Similarity 95.7%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RNPDDGVGPMAYTTNPKRLDY 23
Db 532 RNPDDGVGPMAYTTNPKRLDY 554
RESULT 2
ID PLMN_MACMU STANDARD; PRT; 810 AA.
AC P12545;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Plasminogen precursor (BC 3.4.21.7).
GN PLG.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxId=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89174660; PubMed=2925643;
RA Tomlinson J.E., McLean J.W., Lawn R.M.;
RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
RT synthesis".
RL J. Biol. Chem. 264:5957-5965(1989).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION
CC AND INFLAMMATION. IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAFVIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. ACTIVATED WITH CATALYTIC AMOUNTS OF STREPTOKINASE.
CC MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
CC INVOLVES ONLY CLEAVAGE AFTER ARG-580, RESULTING IN 2 CHAINS HELD
CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
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CC or send an email to license@isb-sb.ch).
CC -----
CC EMBL: J04697; AAA36901.1; -
CC DR PIR: B30848; B30848.
CC DR PIR: B32869; B32869.
CC DR HSSP: P00747; 1PMK.
CC DR MEROPS: S01.233; -
CC DR InterPro: IPR001314; Chymotrypsin.
CC DR InterPro: IPR000001; Kringle.
CC DR InterPro: IPR003014; PAN.

DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PR000051; Kringle_5.
DR Pfam: PF00024; PAN_1.
DR Pfam: PF00089; Trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR_4.
DR SMART: SM00473; PAN_AP_1.
DR SMART: SM00020; TRYPSIN_1.
DR PROSITE: PS00021; KRINGLE_1; 5.
DR PROSITE: PS00070; KRINGLE_2; 5.
DR PROSITE: PS00240; TRYPSIN_DOM_1.
DR PROSITE: PS00134; TRYPSIN_HIS_1.
DR PROSITE: PS00135; TRYPSIN_SER_1.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Signal.
FT SIGNAL 1 19
FT CHAIN 20 810 PLASMINOGEN.
FT CHAIN 20 580 PLASMIN HEAVY CHAIN A.
FT PEPTIDE 20 96 ACTIVATION PEPTIDE.
FT CHAIN 97 580 PLASMIN SHORT FORM OF CHAIN A.
FT CHAIN 581 810 PLASMIN LIGHT CHAIN B.
FT DOMAIN 103 181 KRINGLE 1.
FT DOMAIN 184 262 KRINGLE 2.
FT DOMAIN 275 352 KRINGLE 3.
FT DOMAIN 377 454 KRINGLE 4.
FT DOMAIN 481 560 KRINGLE 5.
FT DOMAIN 581 810 SERINE PROTEASE.
FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
FT BINDING 136 136 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 136 136 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 158 158 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 172 172 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 432 445 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 445 445 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 134 134 FIBRIN.
FT BINDING 136 136 FIBRIN.
FT DISULFID 49 73 BY SIMILARITY.
FT DISULFID 53 61 BY SIMILARITY.
FT DISULFID 103 181 BY SIMILARITY.
FT DISULFID 124 164 BY SIMILARITY.
FT DISULFID 152 176 BY SIMILARITY.
FT DISULFID 185 262 BY SIMILARITY.
FT DISULFID 188 316 BY SIMILARITY.
FT DISULFID 206 245 BY SIMILARITY.
FT DISULFID 234 257 BY SIMILARITY.
FT DISULFID 275 352 BY SIMILARITY.
FT DISULFID 296 335 BY SIMILARITY.
FT DISULFID 324 347 BY SIMILARITY.
FT DISULFID 377 454 BY SIMILARITY.
FT DISULFID 398 437 BY SIMILARITY.
FT DISULFID 426 449 BY SIMILARITY.
FT DISULFID 481 560 BY SIMILARITY.
FT DISULFID 502 543 BY SIMILARITY.
FT DISULFID 531 555 BY SIMILARITY.
FT DISULFID 567 585 BY SIMILARITY.
FT DISULFID 577 585 BY SIMILARITY.
FT DISULFID 607 623 BY SIMILARITY.
FT DISULFID 699 766 BY SIMILARITY.
FT DISULFID 729 745 BY SIMILARITY.
FT DISULFID 756 784 BY SIMILARITY.
FT CAROHRD 365 365 O-LINKED (GALNAAC...) (BY SIMILARITY).
SQ SEQUENCE 810 AA: 90255 MW; A75ELCS1AIAOF24A CRC64;
Query Match 94.2%; Score 130; DB 1; Length 810;
Best Local Similarity 91.3%; Pred. No. 4e-11;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RNPDDGVGPMAYTTNPKRLDY 23
Db 532 RNPDDGVGPMAYTTNPKRLDY 554

RESULT 3
PLMN_MOUSE STANDARD: PRT: 812 AA.

AC P20918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
GN Plg.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_Taxid=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91184812; PubMed=2081600;
RT Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
RT "Characterization of the cDNA coding for mouse plasminogen and
RT localization of the gene to mouse chromosome 17.";
RT Genomics 8:49-61(1990).
[2]
RN CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RX MEDLINE=95042728; PubMed=7525077;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma.";
RT Cell 79:335-348(1994).
[3]
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
CC GRAFAN FOLLICLE. IT ACTIVATES THE URKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOSINS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
CC NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
CC METASTATIC TUMORS IN VIVO.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
CC INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD
CC TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
CC ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY. PLASMINOGEN SUBFAMILY.
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DR EMBL: J04766; AAA50168.1; -.
DR PIR: A38514; A38514.
DR HSSP: P00747; LPMK.
DR MEROPS: S01.233; -.
DR MGD: MGI:97620; Plg.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringlet.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00051; kringlet.5.

Pfam: PF00024; PAN: 1.
DR Pfam: PF00089; trypsin: 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR: 5.
DR SMART: SM00473; PAN_AD: 1.
DR SMART: SM00020; TRYP_Spc: 1.
DR PROSITE: PS00021; KRINGLE_1: 4.
DR PROSITE: PS50070; KRINGLE_2: 5.
DR PROSITE: PS50240; TRYPsin_DOM: 1.
DR PROSITE: PS00134; TRYPsin_HIS: 1.
DR PROSITE: PS00135; TRYPsin_SER: 1.
KW Hydrolyse: Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Signal.
FT SIGNAL 1 19
FT CHAIN 20 812 PLASMINOGEN.
FT CHAIN 20 581 ACTIVATION PEPTIDE.
FT PEPTIDE 20 97 PLASMIN SHORT FORM OF CHAIN A.
FT CHAIN 98 581 ANGIOSTATIN.
FT CHAIN 98 7436 PLASMIN LIGHT CHAIN B.
FT CHAIN 582 812 KRINGLE 1.
FT DOMAIN 103 181 KRINGLE 2.
FT DOMAIN 184 262 KRINGLE 3.
FT DOMAIN 275 352 KRINGLE 4.
FT DOMAIN 377 454 KRINGLE 5.
FT DOMAIN 481 560 SERINE PROTEASE.
FT DOMAIN 582 812 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 624 624 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 667 667 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 762 762 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 49 73 BY SIMILARITY.
FT DISULFID 53 61 BY SIMILARITY.
FT DISULFID 103 181 BY SIMILARITY.
FT DISULFID 124 164 BY SIMILARITY.
FT DISULFID 152 176 BY SIMILARITY.
FT DISULFID 185 262 BY SIMILARITY.
FT DISULFID 188 316 BY SIMILARITY.
FT DISULFID 206 245 BY SIMILARITY.
FT DISULFID 234 257 BY SIMILARITY.
FT DISULFID 275 352 BY SIMILARITY.
FT DISULFID 296 335 BY SIMILARITY.
FT DISULFID 324 347 BY SIMILARITY.
FT DISULFID 377 454 BY SIMILARITY.
FT DISULFID 398 437 BY SIMILARITY.
FT DISULFID 426 449 BY SIMILARITY.
FT DISULFID 481 560 BY SIMILARITY.
FT DISULFID 502 543 BY SIMILARITY.
FT DISULFID 531 553 BY SIMILARITY.
FT DISULFID 568 687 INTERCHAIN (BY SIMILARITY).
FT DISULFID 578 586 INTERCHAIN (BY SIMILARITY).
FT DISULFID 609 625 BY SIMILARITY.
FT DISULFID 701 768 BY SIMILARITY.
FT DISULFID 731 747 BY SIMILARITY.
FT DISULFID 758 786 BY SIMILARITY.
SQ SEQUENCE 812 AA; 90846 MW; D34A74A4FC226F8 CRC64;
Query Match 92.8%; Score 128; DB 1; Length 812;
Best Local Similarity 91.3%; Pred. No. 7.7e-11;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 RNPDSGVGSPWATYTPRKLVDY 23
Db 532 RNPDSGVNGSPWCYTPRKLVDY 554
RESULT 4
PLMN_SHEEP STANDARD: PRT: 343 AA.
AC P81286;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).

GN PLG.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93149995; PubMed=1492092;
 RA Schaller J., Straub C., Kampfer U., Rickli E.E.;
 RT "Complete amino acid sequence of ovine plasminogen."
 RL Protein Seq. Data Anal. 5:21-25(1992).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION. IT WEAKENS THE WALLS OF THE
 GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS AT LEAST 2 KRINGLE DOMAINS.
 DR HSP: P00747; 5HP.
 DR MEROPS: S01.233; -.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; kringle; 1.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00089; Trypsin; 1.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00021; KRINGLE.1; 1.
 DR PROSITE: PS50070; KRINGLE.2; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KM Hydrolyase; Serine protease; Plasma; glycoprotein; fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; zymogen.
 FT NON_TER 1 1
 FT DOMAIN <1 140 HEAVY CHAIN A.
 FT DOMAIN 141 >343 LIGHT CHAIN A.
 FT DOMAIN <1 17 KRINGLE 4.
 FT DOMAIN 41 120 KRINGLE 5.
 FT DOMAIN 114 341 SERINE PROTEASE.
 FT ACT_SITE 181 181 CHARGE RELAY SYSTEM.
 FT ACT_SITE 224 224 CHARGE RELAY SYSTEM.
 FT ACT_SITE 319 319 CHARGE RELAY SYSTEM.
 FT NON_TER 343 343
 SQ SEQUENCE 343 AA; 37662 MW; 8DFEBA92D596EE0 CRC64;
 Query Match 89.9%; Score 124; DB 1; Length 343;
 Best Local Similarity 87.0%; Pred. No. 1.2e-10;
 Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OS Erinaceus europaeus (Western European hedgehog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
 NCBI_TaxID=9365;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96025778; PubMed=7592597;
 RA Lann R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
 RA Byrne C.D., Fong K.J., Meer K., Pathy L.;
 RT "The recurring evolution of lipoprotein(a). Insights from cloning of
 hedgehog apolipoprotein(a)."
 RL J. Biol. Chem. 270:24004-24009(1995).
 RN [2]
 RP REVISIONS.
 RA Lann R.M.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U33171; AAC48717.1; -.
 DR HSP: P00747; 1PMK.
 DR MEROPS: S01.233; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00130; KRINGLE.
 DR SMART: SM00130; KR; 5.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00021; KRINGLE.1; 5.
 DR PROSITE: PS50070; KRINGLE.2; 5.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KM Hydrolyase; Serine protease; Plasma; glycoprotein; fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; zymogen; signal.
 FT SIGNAL 1 19
 FT CHAIN 20 810 PLASMINOGEN.
 FT CHAIN 810 582 PLASMIN HEAVY CHAIN A (BY SIMILARITY).
 FT CHAIN 583 810 PLASMIN LIGHT CHAIN B (BY SIMILARITY).
 FT DOMAIN 103 181 SERINE PROTEASE.
 FT DOMAIN 185 181 KRINGLE 1.
 FT DOMAIN 275 352 KRINGLE 2.
 FT DOMAIN KRINGLE 3.

FT DOMAIN 379 456 KRINGLE 4.
 FT DOMAIN 561 KRINGLE 5.
 FT ACT SITE 482 622 CHARGE RELAY SYSTEM.
 FT ACT SITE 665 665 CHARGE RELAY SYSTEM.
 FT ACT SITE 760 760 CHARGE RELAY SYSTEM.
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 810 AA: 90902 MW: 8E75780946017A16 CRC64;
 Query Match 87.0%; Score 120; DB 1; Length 810;
 Best Local Similarity 82.6%; Pred. No. 11e-09;
 Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RNDGDVGPMWATYTPRKLYDY 23
 Db 533 RNDGDGANGPMWATYTPRKLYDY 555
 RESULT 6
 ID APOA_HUMAN STANDARD; PRT; 4548 AA.
 AC P08519;
 DT 01-AUG-1988 (Rel. 08. Created)
 DT 01-AUG-1988 (Rel. 08. Last sequence update)
 DT 01-MAR-2002 (Rel. 41. Last annotation update)
 DE Apolipoprotein(a) precursor (BC 3.4.21.-) (Apo(a)) (IPI(a)).
 GN LPA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=88039109; PubMed=3670400;
 RA McLean J.W., Tomlison J.E., Kuang W.-J., Eaton D.L., Chen E.Y.,
 RA Pless G.M., Scannu A.M., Lawn R.M.;
 RT "cDNA sequence of human apolipoprotein(a) is homologous to
 RT plasminogen".
 RL Nature 330:132-137(1987).
 RN [2]
 RP SERINE PROTEASE ACTIVITY.
 RA MEDLINE=90076123; PubMed=2531657;
 RA Salonen E.-M., Jauhainen M., Zardi L., Vaheri A., Ehnholm C.;
 RT "Lipoprotein(a) binds to fibrinogen and has serine proteinase
 RT activity capable of cleaving it".
 RL EMBO J. 8:4035-4040(1989).
 RN [3]
 RP REVIEW.
 RA MEDLINE=90049223; PubMed=2530631;
 RA Utermann G.;
 RT "The mysteries of lipoprotein(a)".
 RL Science 246:904-910(1989).
 RN [4]
 RP CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.
 RA MEDLINE=21303595; PubMed=11294842;
 RA Garner B., Merry A.H., Royle L., Harvey D.J., Rudd P.M., Thillet J.;
 RT "Structural elucidation of the N- and O-glycans of human
 RT apolipoprotein(a): role of O-glycans in conferring protease
 RT resistance".
 RL J. Biol. Chem. 276:22200-22208(2001).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.
 RA MEDLINE=96217891; PubMed=8642595;
 RA Michel V., Lograsso P.V., Boettcher B.R.;
 RT "Crystal structures of apolipoprotein(a) kringle IV37 free and
 RT complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic
 RT acid: existence of novel and expected binding modes".
 RL J. Mol. Biol. 256:751-761(1996).
 RN [6]
 RP VARIANT ARG-4193.
 RA MEDLINE=95002201; PubMed=7918682;
 RA Scannu A.M., Pfaffinger D., Lee J.C., Hinman J.;
 RT "A single point mutation (Trp72->Arg) in human apo(a) kringle 4-37
 RT associated with a lysine binding defect in Lp(a)".

RL Biochim. Biophys. Acta 1227:41-45(1994).
 CC -I- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
 CC (Lp(a)). It has serine proteinase activity and is able of
 CC autoproteolysis. Inhibits tissue-type plasminogen activator 1.
 CC Lp(a) may be a ligand for megalin/5p 330.
 CC -I- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibrinogen and
 CC decorin.
 CC -I- PTM: N- and O-glycosylated. The N-glycans are complex biantennary
 CC structures present in either a mono- or disialylated state. The
 CC O-glycans are mostly (80%) represented by the monosialylated core
 CC type I structure, NeuNAcGalpha2-3Galbeta1-3GalNAc, with smaller
 CC amounts of disialylated and non-sialylated O-glycans also
 CC detected.
 CC -I- DISEASE: Elevated plasma concentrations of apo(a) and its
 CC naturally occurring proteolytic fragments is correlated with
 CC atherosclerosis. Homology with plasminogen kringle IV and V is
 CC thought to underlie the atherogenicity of the protein, because the
 CC fragments are competing with plasminogen for fibrin(ogen) binding.
 CC -I- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
 CC leading to the formation of the so called mini-Lp(a). Apo(a)
 CC fragments accumulate in atherosclerotic lesions, where they may
 CC promote thrombogenesis. O-glycosylation may limit the extent of
 CC proteolytic fragmentation.
 CC -I- SIMILARITY: CONTAINS 38 KRINGLE DOMAINS.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY PLASMINOGEN SUBFAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: X06290; CAA29618.1; -
 CC PIR: S00657; S00657.
 CC HSP: P00747; IPMK.
 CC MEROPS: S01.226; -
 CC MIM: 152200; -
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR000001; Kringle.
 CC InterPro: IPR001254; Trypsin.
 CC Pfam: PF00051; kringle; 38.
 CC Pfam: PF00089; trypsin; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00018; KRINGLE.
 CC SMART: SM00130; KR; 38.
 CC SMART: SM00020; TRYPSIN; 1.
 CC PROSITE: PS00021; KRINGLE_1; 38.
 CC PROSITE: PS00070; KRINGLE_2; 38.
 CC PROSITE: PS00240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC HydroLase: Serine protease; Lipid transport; Plasma; Glycoprotein;
 CC Kringle; Repeat; Atherosclerosis; Signal; Polymorphism.
 CC SIGNAL 1 19
 CC CHAIN 20 4548
 CC FT DOMAIN 20 130 KRINGLE TYPE IV, 1.
 CC FT DOMAIN 131 244 KRINGLE TYPE IV, 2.
 CC FT DOMAIN 245 358 KRINGLE TYPE IV, 3.
 CC FT DOMAIN 359 472 KRINGLE TYPE IV, 4.
 CC FT DOMAIN 473 586 KRINGLE TYPE IV, 5.
 CC FT DOMAIN 587 700 KRINGLE TYPE IV, 6.
 CC FT DOMAIN 701 814 KRINGLE TYPE IV, 7.
 CC FT DOMAIN 815 928 KRINGLE TYPE IV, 8.
 CC FT DOMAIN 929 1042 KRINGLE TYPE IV, 9.
 CC FT DOMAIN 1043 1156 KRINGLE TYPE IV, 10.
 CC FT DOMAIN 1157 1270 KRINGLE TYPE IV, 11.
 CC FT DOMAIN 1271 1384 KRINGLE TYPE IV, 12.
 CC FT DOMAIN 1385 1498 KRINGLE TYPE IV, 13.
 CC FT DOMAIN 1499 1612 KRINGLE TYPE IV, 14.
 CC FT DOMAIN 1613 1726 KRINGLE TYPE IV, 15.

RESULT 7	PLMN_HORSE	STANDARD;	PRT;	338 AA.
ID	PLMN_HORSE			
AC	P80010;			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Plasminogen (EC 3.4.21.7) (Fragment).			
GN	PLG.			
OS	Equus caballus (Horse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			
OX	NCBI_TaxID=9796;			
RN	[1]			
RP	SEQUENCE.			
RP	TISSUE=Plasma;			
RX	MEDLINE=92052077; PubMed=1946332;			
RA	Schaller J., Straub C., Kaemfer U., Rickli E.E.;			
RT	"Complete amino acid sequence of equine miniplasminogen.";			
RL	Protein Seq. Data Anal. 4:69-74(1991).			
CC	-1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS			
CC	A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING			
CC	EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,			
CC	AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE			
CC	GRAAFIAN FOLLICLE. IT ACTIVATES THE URINKINASE-TYPE PLASMINOGEN			
CC	ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH			
CC	AS C1 AND C3, IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,			
CC	LAMININ AND VON WILLEBRAND FACTOR.			
CC	-1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN			
CC	ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO			
CC	FIBRIN. ACTIVATED BY CATALYTIC AMOUNTS OF STREPTOKINASE.			
CC	-1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN			

CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC	TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
CC	-1- SIMILARITY: CONTAINS AT LEAST 1 KRINGLE DOMAIN.
DR	PIR; SI7527; SI7527.
DR	HSSP; P00747; 5HPg.
DR	MEROPS; S01.233; -.
DR	InterPro: IPR000001; Kringle.
DR	InterPro: IPR001254; Trypsin.
DR	Pfam; PF00051; kringle; 1.
DR	Pfam; PF00089; trypsin; 1.
DR	SMART; SM00130; KR; 1.
DR	SMART; SM00020; TRYP_SPE; 1.
DR	PROSITE; PS00021; KRINGLE_1; 1.
DR	PROSITE; PS0070; KRINGLE_2; 1.
DR	PROSITE; PS0240; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
KW	Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW	Tissue remodeling; Blood coagulation; Kringle; Zymogen.
FT	NON_TER 1 1
FT	CHAIN <1 108 PLASMIN HEAVY CHAIN A.
FT	CHAIN 109 338 PLASMIN LIGHT CHAIN B.
FT	DOMAIN 9 88 KRINGLE 5.
FT	DOMAIN 109 338 SERINE PROTEASE.
FT	DISULFID 9 88 BY SIMILARITY.
FT	DISULFID 30 71 BY SIMILARITY.
FT	DISULFID 59 83 BY SIMILARITY.
FT	DISULFID 95 213 INTERCHAIN (BY SIMILARITY).
FT	DISULFID 105 113 INTERCHAIN (BY SIMILARITY).
FT	DISULFID 135 151 BY SIMILARITY.
FT	DISULFID 227 294 BY SIMILARITY.
FT	DISULFID 257 273 BY SIMILARITY.
FT	DISULFID 284 312 BY SIMILARITY.
FT	ACT_SITE 150 150 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE 193 193 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE 288 288 STREPTOKINASE-BINDING SITE (PROBABLE).
FT	ACT_SITE 157 157 STREPTOKINASE-BINDING SITE (PROBABLE).
FT	SITE 191 191 STREPTOKINASE-BINDING SITE (PROBABLE).
FT	SITE 269 269 SITE OF SUBSTRATE SPECIFICITY
FT	SITE 282 282 (BY SIMILARITY).
SO	SEQUENCE 338 AA; 37132 MW; 8BEB56B5C5CBB01 CRC64;
QY	Query Match 82.6%; Score 114; DB 1; Length 338;
QY	Best Local Similarity 78.3%; Pred. No. 3.3e-09;
QY	Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY	1 RNPGDYGVGPWATTTNPKRLDY 23
QY	
Db	60 RNPGDVNGPWCYTMNPOKLFDY 82
RESULT 8	
PLMN_PIG	STANDARD; PRT; 790 AA.
AC	P06867;
DT	01-JAN-1988 (Rel. 06, Created)
DT	16-FEB-1991 (Rel. 17, last sequence update)
DT	16-OCT-2001 (Rel. 40, last annotation update)
DE	Plasminogen (EC 3.4.21.7).
OS	Sus scrofa (Pig).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX	NCBI_TaxID=9823;
RM	[1]
RP	SEQUENCE OF 1-560.
RA	Schaller J., Merli T., Roessellet S.J., Kaempfer U., Rickli E.E.;
RT	"Amino acid sequence of the heavy chain of porcine plasmin. Comparison
RT	of the carbohydrate attachment sites with the human and bovine
RT	species";
RL	Fibrinolysis 1:91-102(1987).
RN	[2]

RP SEQUENCE OF 450-790.
 RX MEDLINE-85203907; PubMed-3846533;
 RA Marti T., Schaller J., Rickli E.E.;
 RT "Determination of the complete amino-acid sequence of porcine
 RT miniplasminogen.";
 RL Eur. J. Biochem. 149:279-285(1985).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE-88185329; PubMed-3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to stialylation and
 RT fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- PTM: N-LINKED GLYCANS CONTAINS N-ACETYLGLUCOSAMINE, SIALIC ACID AND
 CC IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAc
 CC DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
 CC (MICROHETEROGENEITY).
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: BELONGS TO KRINGLE DOMAINS.
 CC PIR: A25834; A25834.
 DR PIR: S03733; S03733.
 DR HSSP: P00747; SHP.
 DR MEROPS: S01.233; -.
 DR GlycoSuiteDB: P06867; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; Kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 5.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; TRY_SPE; 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS00070; KRINGLE_2; 5.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
 DR PROSITE: PS00133; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen.
 FT CHAIN 1 560
 FT CHAIN 561 790
 FT DOMAIN 561 790 PLASMIN HEAVY CHAIN A.
 FT DOMAIN 561 790 SERINE PROTEASE.
 FT DOMAIN 84 162 KRINGLE 1.
 FT DOMAIN 166 243 KRINGLE 2.
 FT DOMAIN 256 333 KRINGLE 3.
 FT DOMAIN 358 435 KRINGLE 4.
 FT DOMAIN 461 540 KRINGLE 5.
 FT ACT_SITE 602 602 CHANGE RELAY SYSTEM.
 FT ACT_SITE 645 645 CHANGE RELAY SYSTEM.
 FT ACT_SITE 740 740 CHANGE RELAY SYSTEM.
 FT CARBOHYD N-LINKED (GLCNAC. . .).
 FT /FTid-CAR_000019.

FT CARBOHYD 340 340 O-LINKED (GLCNAC. . .).
 FT MEDLINE-88185329; PubMed-3356193;
 FT /FTid-CAR_000020.
 SQ SEQUENCE 790 AA; 88592 MW; F04FA06F74BCD58E CR664;
 Query Match 81.9%; Score 113; DB 1; Length 790;
 Best Local Similarity 78.3%; Pred. No. 1; le-08;
 Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RNPGDVGGPWAYTNPRIKLYD 23
 DB 512 RNPGDVGGPWCYTTNPQKLDY 534
 RESULT 9
 ID PLMN_BOVIN STANDARD; PRT; 812 AA.
 AC P06868; Q28162;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7).
 GN pig.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Berglund L., Andersen M.D., Petersen T.E.;
 RT "Cloning and characterization of the bovine plasminogen cDNA.";
 RL Int. Dairy J. 5:593-603(1995).
 RN [2]
 RP SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE-85203906; PubMed-3846532;
 RA Schaller J., Moser P.W., Danneberger-Muller G.A.K., Rosselet S.J.,
 RA Kamper U., Rickli E.E.;
 RT "Complete amino acid sequence of bovine plasminogen. Comparison with
 RT human plasminogen.";
 RL Eur. J. Biochem. 149:267-278(1985).
 RN [3]
 RP SEQUENCE OF 706-812 FROM N.A.
 RX MEDLINE-85023311; PubMed-6148961;
 RA Malinowski D.P., Sadler J.E., Davie E.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 RT human and bovine plasminogen.";
 RL Biochemistry 23:4243-4250(1984).
 RN [4]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE-88185329; PubMed-3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to stialylation and
 RT fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 CC AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
 CC GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZMOGENS, SUCH
 CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 CC LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 CC ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 CC FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- PTM: N-LINKED GLYCANS CONTAIN N-ACETYLGLUCOSAMINE AND SIALIC ACID.
 CC O-LINKED GLYCANS CONSIST OF GAL-GALNAc DISACCHARIDE WITH IS
 CC MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY. PLASMINOGEN SUBFAMILY.
CC -----
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CC -----
DR EMBL: X79402; CAAS5939.1; -.
DR EMBL: K02935; AAA30714.1; -.
DR PIR: A25835; PLBO.
DR HSSP: P00747; 2PK4.
DR MEROPS: S01.233; -.
DR Glycosylated; P06866; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00051; Kringle; 5.
DR Pfam: PF00024; PAN; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00130; KR: 5.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS00021; KRINGLE_1; 5.
DR PROSITE: PS50070; KRINGLE_2; 5.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Signal.
FT SIGNAL 1 26
FT CHAIN 27 812 PLASMINOGEN.
FT CHAIN 27 583 PLASMIN HEAVY CHAIN A.
FT CHAIN 584 812 PLASMIN LIGHT CHAIN B.
FT DOMAIN 110 188 KRINGLE 1.
FT DOMAIN 192 269 KRINGLE 2.
FT DOMAIN 282 359 KRINGLE 3.
FT DOMAIN 384 461 KRINGLE 4.
FT DOMAIN 485 564 KRINGLE 5.
FT DOMAIN 584 812 SERINE PROTEASE.
FT CARBOHYD 315 N-LINKED (GLCNAC. . .).
FT CARBOHYD 315 /FTID-CAR_000014.
FT CARBOHYD 365 /FTID-CAR_000015.
FT ACT_SITE 624 624 /FTID-CAR_000015.
FT ACT_SITE 667 667 O-LINKED (GALNAC. . .).
FT ACT_SITE 762 762 CHARGE RELAY SYSTEM.
FT CONFLICT 335 335 CHARGE RELAY SYSTEM.
FT CONFLICT 516 516 N -> D (IN REF. 2).
FT CONFLICT 555 555 Q -> H (IN REF. 2).
FT CONFLICT 744 744 P -> L (IN REF. 2).
FT CONFLICT 744 744 T -> R (IN REF. 3).
SQ SEQUENCE 812 AA; 91216 MW; 38A6AA691E220946 CRC64;

Query Match 80.4%; Score 111; DB 1; Length 812;
Best Local Similarity 78.3%; Prec. No. 2,2e-08;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

07 1 RNPQDVGCPWATYTNPKKLDY 23
Db 536 RNPQDVGCPWATYTNPKKLDY 558

RESULT 10
PLAN CANFA STANDARD; PRT; 333 AA.

AC P80009;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (fragment).
GN PLG.
OS Enkai familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE-Plasma;
RX MEDLINE=90175323; PubMed=2626424;
RA Schaller J, Straub C, Kaempfer U, Rickli E.F.;
RL "Complete amino acid sequence of canine miniplasminogen.";
RT Protein Seq. Data Anal. 2:445-450(1989).
CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC AND INFLAMMATION. IT WEAKENS THE WALLS OF THE
CC GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC LAMININ AND VON WILLEBRAND FACTOR.
CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC ACTIVATORS. BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC FIBRIN. ACTIVATED WITH UROKINASE AND HIGH CONCENTRATIONS OF
CC STREPTOKINASE.
CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY. PLASMINOGEN SUBFAMILY.
CC -1- SIMILARITY: CONTAINS AT LEAST 1 KRINGLE DOMAIN.
DR HSSP: P00747; 5PK4.
DR MEROPS: S01.233; -.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00051; Kringle; 1.
DR Pfam: PF00089; trypsin; 1.
DR SMART: SM00130; KR: 1.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS50070; KRINGLE_2; 1.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolyase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen.
FT NON_TER 1 1
FT CHAIN <1 103 PLASMIN HEAVY CHAIN A.
FT CHAIN 104 333 PLASMIN LIGHT CHAIN B.
FT DOMAIN 4 83 KRINGLE 5.
FT DISULFID 104 333 SERINE PROTEASE.
FT DISULFID 4 83 BY SIMILARITY.
FT DISULFID 25 66 BY SIMILARITY.
FT DISULFID 54 78 BY SIMILARITY.
FT DISULFID 90 208 INTERCHAIN (BY SIMILARITY).
FT DISULFID 100 108 INTERCHAIN (BY SIMILARITY).
FT DISULFID 130 146 BY SIMILARITY.
FT DISULFID 222 289 BY SIMILARITY.
FT DISULFID 252 268 BY SIMILARITY.
FT DISULFID 279 307 BY SIMILARITY.
FT ACT_SITE 145 145 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 188 188 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 283 283 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT SITE 152 152 STREPTOKINASE-BINDING SITE (PROBABLE).
FT SITE 186 186 STREPTOKINASE-BINDING SITE (PROBABLE).
FT SITE 264 264 STREPTOKINASE-BINDING SITE (PROBABLE).
FT SITE 277 277 SITE OF SUBSTRATE SPECIFICITY (BY SIMILARITY).
SQ SEQUENCE 333 AA; 36678 MW; C8C0271B6C6AC8D4 CRC64;

RC STRAIN-BALB/C; TISSUE=Liver;
 RA MEDLINE=92002017; PubMed=1832957;
 RX Friener Degen S.J., Stuart L.A., Han S., Jamison C.S.;
 RT "Characterization of the mouse cDNA and gene coding for a hepatocyte
 growth factor-like protein: expression during development.";
 RL Biochemistry 30:9781-9791(1991).
 CC -1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL AA
 CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
 CONSERVED.
 CC -1- TISSUE SPECIFICITY: LIVER. LOWER LEVELS IN LUNG, PLACENTA AND
 ADRENAL.
 CC -1- DEVELOPMENTAL STAGE: IS EXPRESSED AT LOW LEVELS DURING GESTATION.
 CC JUST BEFORE BIRTH THE LEVEL INCREASES DRAMATICALLY AND REMAINS
 CC STABLE AFTERWARDS.
 CC -1- PTM: MAY BE CLEAVED AFTER AA 488, TO YIELD A TWO-CHAIN MOLECULE
 CC HELD TOGETHER BY DISULFIDE BONDS, OR CLEAVED INTO TWO SEPARATE
 CC POLYPEPTIDES.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY, PLASMINOGEN SUBFAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M74180; AAA50166.1; -;
 DR EMBL: M74181; AAA50167.1; -;
 DR HSSP: P00747; IKRN.
 DR MEDOPS: S01.975; -;
 DR MGP: MGI:96080; Hgfl.
 DR Interpro: IPR001314; Chymotrypsin.
 DR Interpro: IPR000001; Kringle.
 DR Interpro: IPR003014; PAN.
 DR Interpro: IPR003609; Pan_app.
 DR Pfam: PF00051; Kringle; 4.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 4.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS00021; KRINGLE_1; 4.
 DR PROSITE: PS00070; KRINGLE_2; 4.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR Kringle; Glycoprotein; Serine protease homolog; Signal.
 KW Kringle; Glycoprotein; Serine protease homolog; Signal.
 FT SIGNAL 1 18
 FT CHAIN 1 716
 FT DOMAIN 19 109
 FT DOMAIN 110 186
 FT DOMAIN 191 268
 FT DOMAIN 292 370
 FT DOMAIN 379 457
 FT DOMAIN 489 716
 FT DISULFID 56 78
 FT DISULFID 60 66
 FT DISULFID 110 186
 FT DISULFID 131 169
 FT DISULFID 157 181
 FT DISULFID 191 268
 FT DISULFID 194 333
 FT DISULFID 212 251
 FT DISULFID 240 263
 FT DISULFID 292 370
 FT DISULFID 313 352
 FT DISULFID 341 364
 FT DISULFID 379 457
 FT DISULFID 400 440
 FT DISULFID 400 440

FT DISULFID 428 452 BY SIMILARITY.
 FT DISULFID 477 593 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 512 528 BY SIMILARITY.
 FT DISULFID 607 672 BY SIMILARITY.
 FT DISULFID 637 651 BY SIMILARITY.
 FT DISULFID 662 690 BY SIMILARITY.
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 19 19 P -> Q (IN GENOMIC SEQUENCE).
 SQ SEQUENCE 716 AA; 80588 MW; BDC02EF85213ACC CRC64;
 Qy 1 RNPDSGVGPMWYTTNPKRLDY 23
 Db 429 RNPDSHSGPMCYTLDPDLFDY 451
 RESULT 13
 HGF_RAT
 ID HGF_RAT STANDARD: PRT; 728 AA.
 AC P17945;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Hepatocyte growth factor precursor (Scatter factor) (SF)
 DE (Hepatopoietin A).
 DE HGF.
 GN HGF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=WISTAR; TISSUE=Liver;
 RX MEDLINE=90222197; PubMed=2139229;
 RA Toshito K., Hagiya M., Nishizawa T., Seki T., Shimonishi M.,
 RA Shimizu S., Nakamura T.;
 RT "Reduced primary structure of rat hepatocyte growth factor and
 RT expression of the mRNA in rat tissues.";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=Liver;
 RX MEDLINE=91031482; PubMed=2146117;
 RA Okajima A., Miyazawa K., Kitamura N.;
 RT "Primary structure of rat hepatocyte growth factor and induction of
 RT its mRNA during liver regeneration following hepatic injury.";
 RT Eur. J. Biochem. 193:375-381(1990).
 CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
 CC HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPIC FACTOR, AND ACTS
 CC AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
 CC IT HAS NO DETECTABLE PROTEASE ACTIVITY.
 CC -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
 CC DISULFIDE BOND.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY, PLASMINOGEN SUBFAMILY.
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 CC -----
 DR EMBL: D90102; BAA14133.1; -;
 DR EMBL: X54400; CAA38266.1; -;

DR PIR: S13211; S13211.
 DR PIR: A35644; A35644.
 DR HSSP: P14210; 1BHT.
 DR MEROPS: S01.978; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringles.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan_app.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; kringles; 4.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00130; KR; 4.
 DR SMART: SM00473; PAN_AP; 1.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00021; KRINGLE_1; 4.
 DR PROSITE: PS50070; KRINGLE_2; 4.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 KW Growth factor; Kringles; Glycoprotein; Serine protease homolog;
 KW Signal.
 FT SIGNAL 1 32 BY SIMILARITY.
 FT CHAIN 33 495 HEPATOCYTE GROWTH FACTOR ALPHA CHAIN.
 FT CHAIN 496 728 HEPATOCYTE GROWTH FACTOR BETA CHAIN.
 FT MOD_RES 33 33 PYRROLIDONE CARBOXYLIC ACID
 (BY SIMILARITY).
 FT DOMAIN 33 128 PAP.
 FT DOMAIN 129 207 KRINGLE 1.
 FT DOMAIN 212 289 KRINGLE 2.
 FT DOMAIN 306 384 KRINGLE 3.
 FT DOMAIN 392 470 KRINGLE 4.
 FT DOMAIN 496 728 SERINE PROTEASE-LIKE.
 FT DISULFID 71 97 BY SIMILARITY.
 FT DISULFID 75 85 BY SIMILARITY.
 FT DISULFID 488 607 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 656 656 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 728 AA; 82905 MW; 3E0BF1F96ADCEDEF CRC64;
 Query Match 59.4%; Score 82; DB 1; Length 728;
 Best Local Similarity 60.9%; Pred. No. 0.0003;
 Matches 14; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 OY 1 RNPDDGVGPFWATYTPKRLYDT 23
 DB 442 RNPDDAHGFWCYTGNPLVPMWY 464
 RESULT 14
 HGF_HUMAN STANDARD: PRT; 728 AA.
 ID HGF_HUMAN
 AC P14210; Q9DDU6; Q9BYL9;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1991 (Rel. 19, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Hepatocyte growth factor precursor (Scatter factor) (SF)
 DE (Hepatopoietin A).
 GN HGF OR HPTA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 ON [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91340155; PubMed=1831432;
 RA Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;
 "Organisation of the human hepatocyte growth factor-encoding gene.";
 RL Gene 102:213-219(1991).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=89392017; PubMed=2528952;
 RA Miyazawa K., Tsubouchi H., Naka D., Takahashi K., Okigaki M.,
 RA Arakaki N., Nakayama H., Hiroto S., Sakiyama O., Takahashi K.,
 RA Gohda E., Daikuhara Y., Kitamura N.;
 "Molecular cloning and sequence analysis of cDNA for human hepatocyte
 growth factor.";
 RT Biochem. Biophys. Res. Commun. 163:967-973(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=91025062; PubMed=2145836;
 RA Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa T.,
 RA Asami O., Hagiya M., Nakamura T., Shimizu S.;
 "Isolation and expression of cDNA for different forms of hepatocyte
 growth factor from human leukocyte.";
 RT Biochem. Biophys. Res. Commun. 172:321-327(1990).
 RL [4]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 55-73 AND 495-520.
 RC TISSUE=Liver;
 RX MEDLINE=90066676; PubMed=2531289;
 RA Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimonishi M.,
 RA Sugimura A., Tashiro K., Shimizu S.;
 "Molecular cloning and expression of human hepatocyte growth factor.";
 RL Nature 342:440-443(1989).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic Fibroblast;
 RX MEDLINE=9134393; PubMed=1831266;
 RA Weidner K.M., Arakaki N., Hartmann G., Vandekerckhove J., Weingart S.,
 RA Rieder H., Fönetsch C., Tsubouchi H., Hishida T., Daikuhara Y.,
 RA Birchemier W.;
 "Evidence for the identity of human scatter factor and human
 hepatocyte growth factor.";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005(1991).
 RL [6]
 RP SEQUENCE FROM N.A.
 RC Courtney L., Elliot G., Angel S.;
 submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RL [7]
 RP SEQUENCE OF 249-695 FROM N.A.
 RX MEDLINE=91369928; PubMed=1832556;
 RA Miyazawa K., Kitamura A., Kitamura N.;
 "Structural organization and the transcription initiation site of the
 human hepatocyte growth factor gene.";
 RT Biochemistry 30:9170-9176(1991).
 RN [8]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=91207365; PubMed=1826837;
 RA Yoshiyama Y., Arakaki N., Naka D., Takahashi K., Hiroto S., Kondo J.,
 RA Nakayama H., Gohda E., Kitamura N., Tsubouchi H., Ishii T.,
 RA Hishida T., Daikuhara Y.;
 "Identification of the N-terminal residue of the heavy chain of both
 native and recombinant human hepatocyte growth factor.";
 RT Biochem. Biophys. Res. Commun. 175:660-667(1991).
 RL [9]
 RP CARBOHYDRATE-LINKAGE SITE 476.
 RX MEDLINE=93129192; PubMed=1482348;
 RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
 RA Nakamura T., Shimizu S.;
 "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
 on the alpha chain.";
 RT Biochem. Biophys. Res. Commun. 189:1329-1335(1992).
 RL [10]
 RP MUTAGENESIS.
 RX MEDLINE=92331602; PubMed=1321034;
 RA Loker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins K.A.,
 RA Baker J.B., Godowski P.J.;
 "Structure-function analysis of hepatocyte growth factor:
 identification of variants that lack mitogenic activity yet retain
 high affinity receptor binding.";
 RL EMBO J. 11:2503-2510(1992).
 RN [11]

RP STRUCTURE BY NMR OF 31-127.
 RX MEDLINE-98154323; PubMed-9493272;
 RA Zhou H., Mazzulla M.J., Kaufman J.D., Stahl S.J., Wingfield P.T.,
 RT Rubin J.S., Bottaro D.P., Byrd R.A.;
 RT "The solution structure of the N-terminal domain of hepatocyte growth
 RT factor reveals a potential heparin-binding site.";
 RT Structure 6:109-116(1998).
 RL [12]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.
 RX MEDLINE-99036858; PubMed-9817840;
 RA Ulsch M., Lokker N.A., Godowski P.J., de Vos A.M.;
 RT "Crystal structure of the NK1 fragment of human hepatocyte growth
 RT factor at 2.0-A resolution.";
 RT Structure 6:1383-1393(1998).
 CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
 CC HEPATOCTE CELLS. SPEMS TO BE AN HEPATOTROPHIC FACTOR, AND ACTS
 CC AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
 CC IT HAS NO DETECTABLE PROTEASE ACTIVITY.
 CC -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
 CC DISULFIDE BOND.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRIPSIN FAMILY. PLASMINOGEN SUBFAMILY.
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 CC -----
 DR EMBL; D90334; BAA14348.1; JOINED.
 DR EMBL; D90318; BAA14348.1; JOINED.
 DR EMBL; D90319; BAA14348.1; JOINED.
 DR EMBL; D90320; BAA14348.1; JOINED.
 DR EMBL; D90322; BAA14348.1; JOINED.
 DR EMBL; D90323; BAA14348.1; JOINED.
 DR EMBL; D90324; BAA14348.1; JOINED.
 DR EMBL; D90325; BAA14348.1; JOINED.
 DR EMBL; D90326; BAA14348.1; JOINED.
 DR EMBL; D90327; BAA14348.1; JOINED.
 DR EMBL; D90328; BAA14348.1; JOINED.
 DR EMBL; D90329; BAA14348.1; JOINED.
 DR EMBL; D90330; BAA14348.1; JOINED.
 DR EMBL; D90331; BAA14348.1; JOINED.
 DR EMBL; D90332; BAA14348.1; JOINED.
 DR EMBL; D90333; BAA14348.1; JOINED.
 DR EMBL; D90334; BAA14348.1; JOINED.
 DR EMBL; M29145; AAA52650.1; -.
 DR EMBL; M60718; AAA52648.1; -.
 DR EMBL; X16323; CAA34387.1; -.
 DR EMBL; M73239; AAA64239.1; -.
 DR EMBL; M73240; AAA64237.1; -.
 DR EMBL; AC004960; AAC71655.1; -.
 DR EMBL; M75983; AAG53460.1; JOINED.
 DR EMBL; M75972; AAG53460.1; JOINED.
 DR EMBL; M75973; AAG53460.1; JOINED.
 DR EMBL; M75974; AAG53460.1; JOINED.
 DR EMBL; M75975; AAG53460.1; JOINED.
 DR EMBL; M75976; AAG53460.1; JOINED.
 DR EMBL; M75977; AAG53460.1; JOINED.
 DR EMBL; M75978; AAG53460.1; JOINED.
 DR EMBL; M75979; AAG53460.1; JOINED.
 DR EMBL; M75980; AAG53460.1; JOINED.
 DR EMBL; M75981; AAG53460.1; JOINED.
 DR EMBL; M75982; AAG53460.1; JOINED.
 DR PIR; JH0579; JH0579.
 DR PIR; S06794; S06794.
 DR PDB; 2HGF; 24-JUN-98.
 DR PDB; 1BHT; 18-NOV-98.
 DR MEROPS; S01.976; -.
 DR GlycosultedB; P14210; -.
 DR MIM; 142409; -.

DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan. app.
 DR InterPro; IPR001254; Trypsin.
 DR Pfam; PF000051; Kringle; 4.
 DR Pfam; PF000024; PAN; 1.
 DR Pfam; PF000089; Trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0018; KRINGLE.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS00070; KRINGLE_2; 4.
 DR PROSITE; PS02240; TRYPsin_DOM; 1.
 KW Growth factor; Kringle; Glycoprotein; Serine protease homolog;
 KW Signal; 3D-structure.
 FT SIGNAL 1 31
 FT CHAIN 32 494 HEPATOCTE GROWTH FACTOR ALPHA CHAIN.
 FT MOD_RES 32 32 HEPATOCTE GROWTH FACTOR BETA CHAIN.
 FT DOMAIN 32 127 PAP.
 FT DOMAIN 128 206 KRINGLE 1.
 FT DOMAIN 211 288 KRINGLE 2.
 FT DOMAIN 305 383 KRINGLE 3.
 FT DOMAIN 391 469 KRINGLE 4.
 FT DOMAIN 495 728 SERINE PROTEASE-LIKE.
 FT DISULFID 70 96
 FT DISULFID 74 84
 FT DISULFID 128 206
 FT DISULFID 149 189
 FT DISULFID 177 201
 FT DISULFID 487 604 INTERCHAIN (BY SIMILARITY).
 Query Match 58.7%; Score 81; DB 1; Length 728;
 Best Local Similarity 60.9%; Pred. No. 0.00042;
 Matches 14; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 Oy 1 RNPDDVGPMNATYTPKRLDY 23
 Db 441 RNPDDAHGPMCTGNPLIPWDY 463
 RESULT 15
 HGF_MOUSE
 ID HGF_MOUSE STANDARD; PRT; 728 AA.
 AC Q06048; Q64007; Q61662;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hepatocyte growth factor precursor (Scatter factor) (SF)
 DE (Hepatopoietin A).
 GN HGF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 496-504.
 RP TISSUE=Mammary fibroblast;
 RX MEDLINE-94183257; PubMed-8135822;
 RA Sasaki M., Nishio M., Sasaki T., Enami J.;
 RT "Identification of mouse mammary fibroblast-derived mammary growth
 RT factor as hepatocyte growth factor.";
 RL Biochem. Biophys. Res. Commun. 199;772-779(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE-94363381; PubMed-8081873;
 RA Lee C.C., Kozak C.A., Yamada K.M.;
 RT "Structure, genetic mapping, and expression of the mouse Hgf/scatter
 RT factor gene.";

Cell Adhes. Commun. 1:101-111(1993).
 [3]
 RL SEQUENCE FROM N.A.
 RP TISSUE=LIVER;
 RC MEDLINE=94060105; PubMed=8241272;
 RA Iliu Y., Michalopoulos G.K., Zarnegar R.;
 RT "Molecular cloning and characterization of cDNA encoding mouse
 hepatocyte growth factor.";
 RL Biochim. Biophys. Acta 1216:299-303(1993).
 CC -1- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
 HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPIC FACTOR, AND ACTS
 AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
 CC IT HAS NO DETECTABLE PROTEASE ACTIVITY.
 CC -1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
 DISULFIDE BOND.
 CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM OF HGF IS PRODUCED BY
 ALTERNATIVE RNA SPLICING. THE SEQUENCE SHOWN HERE IS THAT OF THE
 LONG FORM.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
 CC -----
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 or send an email to license@sdb.ch).
 CC -----
 CC EMBL; D10212; BAA01064.1; -
 DR EMBL; D10213; BAA01065.1; -
 DR EMBL; S71816; AAB31855.1; -
 DR EMBL; S72307; CAA51054.1; ALT_INIT.
 DR HSSP; P14210; 1BHT.
 DR MGD; MG1:96079; Hgf.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR001254; Trypsin.
 DR Pfam; PF00051; kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO00722; CHYMOTRYPSIN.
 DR PRINTS; PRO0018; KRINGLE.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRYP_Spec; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS50070; KRINGLE_2; 4.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 KW Growth factor; Kringle; Glycoprotein; Serine protease homolog;
 KW Signal; Alternative splicing.
 FT SIGNAL 1 32
 FT CHAIN 33 495 HEPATOCYTE GROWTH FACTOR ALPHA CHAIN.
 FT MOD_RES 456 728 HEPATOCYTE GROWTH FACTOR BETA CHAIN.
 FT MOD_RES 33 33 PYRROLIDONE CARBOXYLIC ACID
 FT MOD_RES (BY SIMILARITY).
 FT DOMAIN 33 128 KRINGLE 1.
 FT DOMAIN 129 207 KRINGLE 2.
 FT DOMAIN 212 289 KRINGLE 3.
 FT DOMAIN 306 384 KRINGLE 4.
 FT DOMAIN 392 470 KRINGLE 4.
 FT DOMAIN 496 728 SERINE PROTEASE-LIKE.
 FT DISULFID 71 97 BY SIMILARITY.
 FT DISULFID 75 85 BY SIMILARITY.
 FT DISULFID 488 607 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 656 656 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 163 167 MISSING (IN SHORT ISOFORM).

FT CONFLICT 344 344 N -> K (IN REF. 2).
 FT CONFLICT 479 479 V -> L (IN REF. 2).
 FT CONFLICT 564 564 R -> H (IN REF. 3).
 SO SEQUENCE 728 AA; 82944 MW; A0381FC49734328 CRC64;
 Query Match 58.7%; Score 81; DB 1; Length 728;
 Best Local Similarity 60.9%; Pred. No. 0.00042;
 Matches 14; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 OY 1 RNPDSGVCPPAAVYTTNPKRLDYD 23
 DB 442 RNPDDAHGPMCTGNPLIPMDY 464
 RESULT 16
 THRB_BOVIN STANDARD; PRT; 625 AA.
 ID THRB_BOVIN
 AC P00735;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5).
 GN F2.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 CX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88245190; PubMed=3379642;
 RA Irvin D.M., Robertson K.A., McGilivray R.T.A.;
 RT "Structure and evolution of the bovine prothrombin gene.";
 RL J. Mol. Biol. 200:31-45(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84203525; PubMed=6326805;
 RA McGilivray R.T.A., Davie E.W.;
 RT "Characterization of bovine prothrombin mRNA and its translation
 product.";
 RL Biochemistry 23:1626-1634(1984).
 RN [3]
 RP SEQUENCE OF 44-625, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RA Magnusson S., Soltup-Jensen L., Petersen T.E., Claes H.;
 RL (Ir) Hemker H.C., Velkamp J.J. (eds.);
 RL Boerhaave symposium on prothrombin and related coagulation factors,
 pp.25-46, Leiden University Press, Leiden (1975).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 RX MEDLINE=86296631; PubMed=3741841;
 RA Park C.H., Tulinsky A.;
 RT "Three-dimensional structure of the kringle sequence: structure of
 prothrombin fragment 1.";
 RL Biochemistry 25:3977-3982(1986).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 RX MEDLINE=91311686; PubMed=1856869;
 RA Seshadri T.-P., Tulinsky A., Skrzypczak-Jankun F., Park C.H.;
 RT "Structure of bovine prothrombin fragment 1 refined at 2.25-A
 resolution.";
 RL J. Mol. Biol. 220:481-494(1991).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 RX MEDLINE=92190185; PubMed=1547228;
 RA Soriano-garcia M., Padmanabhan K., de Vos A.M., Tulinsky A.;
 RT "The Ca2+ ion and membrane binding structure of the Gla domain of Ca-
 prothrombin fragment 1.";
 RL Biochemistry 31:2554-2566(1992).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=92218459; PubMed=1560020;
 RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
 RT "The structure of residues 7-16 of the A alpha-chain of human

RT fibinogen bound to bovine thrombin at 2.3-A resolution.";
 RL J. Biol. Chem. 267:7911-7920(1992).
 [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=92389319; PubMed=1518046;
 RA Brandstetter H., Turk D., Hoeffken H.W., Grosse D., Stuerzebecher J.,
 RA Martin P.D., Edwards B.F.P., Bode W.;
 RT "Refined 2.3 A X-ray crystal structure of bovine thrombin complexes
 RT formed with the benzamide and arginine-based thrombin inhibitors
 RT NAPP, 4-TAPAP and MQPA. A starting point for improving
 RT antithrombotics";
 RL J. Mol. Biol. 226:1085-1089(1992).
 [9]
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.
 RX MEDLINE=97102783; PubMed=8947023;
 RA van de Locht A., Stubbs M.T., Bode W., Friedrich T., Bollschweiler C.,
 RA Hoeffken W., Huber R.;
 RT "The ornithodorin-thrombin crystal structure, a key to the TAP
 RT enigma?";
 RL EMBO J. 15:6011-6017(1996).
 [10]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIABIN.
 RX MEDLINE=96004486; PubMed=9342325;
 RA Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D.,
 RA Huber R., Bode W.;
 RT "Structure of the thrombin complex with triabin, a lipocalin-like
 RT exosite-binding inhibitor derived from a triatomine bug.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
 [11]
 RP GENE STRUCTURE.
 RX MEDLINE=86077733; PubMed=3000440;
 RA Irwin D.M., Ahern K.G., Pearson G.D., McGillivray R.T.A.;
 RT "Characterization of the bovine prothrombin gene.";
 RL Biochemistry 24:6854-6861(1985).
 CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 CC ENZYME. THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CC OF PROTHROMBIN TO THROMBIN.
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 CC THROMBIN.
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -1- DATABASE: NAME=prozyme technical fact sheet;
 CC WWW="http://www.prozyme.com/technical/thrombindata.html".
 CC -----
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 CC -----
 DR EMBL; V00135; CAA23451.1; -;
 DR EMBL; J00041; AAA30781.1; -;
 DR PIR; A00915; TBBO.
 DR PIR; S02537; S02537.

DR	PDB; 1BBR; 31-JAN-94.	
DR	PDB; 1ETR; 31-JAN-94.	
DR	PDB; 1ETI; 31-JAN-94.	
DR	PDB; 1HRT; 31-JAN-94.	
DR	PDB; 2PE1; 31-JAN-94.	
DR	PDB; 2PE2; 31-JAN-94.	
DR	PDB; 2SPT; 31-MAY-94.	
DR	PDB; 1MKX; 07-JUL-97.	
DR	PDB; 1MKA; 07-JUL-97.	
DR	PDB; 1TBQ; 14-OCT-96.	
DR	PDB; 1TBC; 23-JUL-97.	
DR	PDB; 1VIT; 21-APR-97.	
DR	PDB; 1YCP; 06-MAY-98.	
DR	PDB; 1A0H; 17-JUN-98.	
DR	PDB; 1AVG; 16-FEB-99.	
DR	MEROPS; S01.217; -.	
DR	InterPro; IPR001314; Chymotrypsin.	
DR	InterPro; IPR002383; GLA blood.	
DR	InterPro; IPR000001; Kringle.	
DR	InterPro; IPR003966; Prothrombin.	
DR	InterPro; IPR001254; Trypsin.	
DR	InterPro; IPR000294; VitK_dep_GLA.	
DR	Pfam; PF00594; gla; 1.	
DR	Pfam; PF00051; kringle; 2.	
DR	Pfam; PF00089; trypsin; 1.	
DR	PRINTS; PR00722; CHYMOTRYPSIN.	
DR	PRINTS; PR00001; GLABLOOD.	
DR	PRINTS; PR00018; KRINGLE.	
DR	PRINTS; PR01505; PROTHROMBIN.	
DR	SMART; SM00069; GLA; 1.	
DR	SMART; SM00130; KR; 2.	
DR	SMART; SM00020; TRY-SPEC; 1.	
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.	
DR	PROSITE; PS00021; KRINGLE_1; 2.	
DR	PROSITE; PS00070; KRINGLE_2; 2.	
DR	PROSITE; PS00240; TRYPsin_DOM; 1.	
DR	PROSITE; PS00134; TRYPsin_HTS; 1.	
DR	PROSITE; PS00135; TRYPsin_SER; 1.	
KW	Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;	
KW	Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;	
KW	Hydrolase; Serine protease; Kringle; signal; 3D-structure.	
FT	SIGNAL	1 24
FT	PROPEP	25 43
FT	CHAIN	44 625
FT	PEPTIDE	44 199
FT	PEPTIDE	200 317
FT	CHAIN	318 366
FT	CHAIN	367 625
FT	DOMAIN	109 187
FT	DOMAIN	214 292
FT	DOMAIN	367 625
FT	SITE	199 200
FT	SITE	317 318
FT	SITE	366 367
FT	ACT_SITE	409 455
FT	ACT_SITE	465 465
FT	ACT_SITE	571 571
FT	MOD_RES	50 50
FT	MOD_RES	51 51
FT	MOD_RES	58 58
FT	MOD_RES	60 60
FT	MOD_RES	63 63
FT	MOD_RES	64 64
FT	MOD_RES	69 69
FT	MOD_RES	70 70
FT	MOD_RES	73 73
FT	MOD_RES	76 76
FT	CARBOHYD	120 120

Query Match 58.0%; Score 80; DB 1; Length 625;
 Best Local Similarity 70.6%; Pred. No. 0.0005;

Best Local Similarity 70.6%; Pred. No. 0.0026;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 RNPDDGVCSPMAYTNP 17
Db 189 RNPDDGVCSPMAYTNP 205

RESULT 19

THRB RAT STANDARD: PRT: 617 AA.
AC P18252;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN F2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=90332426; PubMed=2377469;
RA Dihanich M., Monard D.;
RT "CDNA sequence of rat prothrombin."
RL Nucleic Acids Res. 18:4251-4251(1990).
[2]
RP SEQUENCE OF 383-617 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
CC ENZYME. THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
CC THROMBIN.
CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
CC BY FACTOR XA.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
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CC -----
DR EMBL: X52835; CA37017.1; -;
DR EMBL: M81397; AAA42240.1; -;
DR PIR: S10511; S10511.
DR HSSP: P00734; IUVS.
DR MEROPS: S01.217; -;

DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000001; kringle.
DR InterPro: IPR003966; Prothrombin.
DR InterPro: IPR001254; Trypsin.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00594; gla_1.
DR Pfam: PF00051; kringle_2.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR SMART: SM00069; GLA_1.
DR SMART: SM00130; KR_2.
DR SMART: SM00020; TRYP-spec_1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS00021; KRINGLE_1; 2.
DR PROSITE: PS00070; KRINGLE_2; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Blood coagulation: Plasma; Calcium-binding; Glycoprotein; Repeat;
KW Vitamin K; zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KW Hydrolyase; Serine protease; Kringle; Signal.
FT SIGNAL 1 24
FT PROPEP 25 43
FT CHAIN 44 617
FT PEPTIDE 44 200
FT PEPTIDE 201 323
FT CHAIN 324 359
FT CHAIN 360 617
FT DOMAIN 109 187
FT DOMAIN 215 292
FT DOMAIN 360 617
FT SITE 200 201
FT SITE 323 324
FT SITE 359 360
FT ACT_SITE 402 402
FT ACT_SITE 458 458
FT ACT_SITE 564 564
FT MOD_RES 50 50
FT MOD_RES 51 51
FT MOD_RES 58 58
FT MOD_RES 60 60
FT MOD_RES 63 63
FT MOD_RES 64 64
FT MOD_RES 69 69
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 76 76
FT CARBOHYD 120 120
FT CARBOHYD 144 144
FT CARBOHYD 412 412
FT CARBOHYD 552 552
FT DISULFID 61 66
FT DISULFID 91 104
FT DISULFID 109 187
FT DISULFID 130 170
FT DISULFID 158 182
FT DISULFID 215 292
FT DISULFID 236 276
FT DISULFID 264 287
FT DISULFID 332 478
FT DISULFID 387 403
FT DISULFID 532 546
FT DISULFID 560 590
SQ SEQUENCE 617 AA; 70411 MW; AD27D1871445DB1D CRC64;

Query Match 52.9%; Score 73; DB 1; Length 617;
Best Local Similarity 64.7%; Pred. No. 0.0051;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 RMPDGVGGPMAYTNP 17
 DB 159 RMPDSTSGPMWCTTDP 175

RESULT 20
 THROMB 20
 ID THROMB 20 STANDARD: PRT: 618 AA.

AC P19221.
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5).
 GN F2 OR CF2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Liver;
 RC MEDLINE=91025551; PubMed=2222810;
 RA Fritzenr Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
 RA Fitzgibbon J.J., Pai J.-A., Chapman V.M., Elliott R.W.;
 RT "Characterization of the cDNA coding for mouse prothrombin and
 RT localization of the gene on mouse chromosome 2.";
 RL DNA Cell Biol. 9:487-498(1990).
 RN [2]
 RP SEQUENCE OF 384-618 FROM N.A.
 RC TISSUE=Liver;
 RC MEDLINE=92212913; PubMed=1557383;
 RA Banfield D.K., Macgillivray R.T.;
 RT "Partial characterization of vertebrate prothrombin cDNAs:
 RT amplification and sequence analysis of the B chain of thrombin from
 RT nine different species.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
 CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 CC AND IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC -1- PTH: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CC OF PROTHROMBIN TO THROMBIN.
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 CC THROMBIN.
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC or send an email to license@isb-slb.ch).
 CC -----
 CC EMBL: X52308; CAA36548.1; -
 CC EMBL: M81394; AAA40435.1; -
 CC PIR: A35827; A35827.
 CC HSSP: P00734; 1B7X.
 CC MEROPS: S01.217; -
 CC MGD: MGI:88380; F2.

DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003966; Prothrombin.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000294; Vitk_dep_GLA.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00051; kringle; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR PRINTS: PRO0001; GLABLOOD.
 DR PRINTS: PRO0018; KRINGLE.
 DR PRINTS: PRO1505; PROTHROMBIN.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00130; KR; 2.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS00011; GLU-CARBOXYLATION; 1.
 DR PROSITE: PS00021; KRINGLE_1; 2.
 DR PROSITE: PS50070; KRINGLE_2; 2.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 KW Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
 KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
 KW Hydrolyase; Serine protease; Kringle; Signal.
 FT SIGNAL 1 24
 FT PROPEP 25 43
 FT CHAIN 44 618
 FT PEPTIDE 44 200
 FT PEPTIDE 201 324
 FT CHAIN 325 360
 FT CHAIN 361 618
 FT DOMAIN 109 187
 FT DOMAIN 215 292
 FT DOMAIN 361 618
 FT SITE 200 201
 FT SITE 324 325
 FT SITE 360 361
 FT ACT_SITE 403 403
 FT ACT_SITE 459 459
 FT ACT_SITE 565 565
 FT MOD_RES 50 50
 FT MOD_RES 51 51
 FT MOD_RES 58 58
 FT MOD_RES 60 60
 FT MOD_RES 63 63
 FT MOD_RES 64 64
 FT MOD_RES 69 69
 FT MOD_RES 70 70
 FT MOD_RES 73 73
 FT MOD_RES 76 76
 FT MOD_RES 91 104
 FT DISULFID 109 187
 FT DISULFID 130 170
 FT DISULFID 158 182
 FT DISULFID 215 293
 FT DISULFID 236 276
 FT DISULFID 264 288
 FT DISULFID 333 479
 FT DISULFID 388 404
 FT DISULFID 533 547
 FT DISULFID 561 591
 FT CARBOHYD 122 122
 FT CARBOHYD 144 144
 FT CARBOHYD 413 413
 FT CARBOHYD 553 553
 FT SEQUENCE 618 AA; 70268 MW; B89F719A9F601E0 CRC64;

Query Match 51.4%; Score 71; DB 1; Length 618;
 Best Local Similarity 64.7%; Pred. No. 0.0099;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNPDGVDGSPWATYTNP 17
 DB 159 RNPDSTGPMCYTTDP 175

RESULT 21
 TRIRB_HUMAN STANDARD; PRT; 622 AA.
 ID TRIRB_HUMAN
 AC P00734;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Prothrombin Precursor (EC 3.4.21.5) (Coagulation factor II).
 GN F2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88077877; PubMed=2825773;
 RA Degen S.J.F., Davie E.W.;
 RT "Nucleotide sequence of the gene for human prothrombin.";
 RL Biochemistry 26:6165-6177(1987).
 RN [2]
 RP SEQUENCE OF 8-622 FROM N.A.
 RX MEDLINE=83231469; PubMed=6305407;
 RA Degen S.J.F., McGillivray R.T.A., Davie E.W.;
 RT "Characterization of the complementary deoxyribonucleic acid and gene
 coding for human prothrombin.";
 RL Biochemistry 22:2087-2097(1983).
 RN [3]
 RP SEQUENCE OF 44-314.
 RX MEDLINE=77193964; PubMed=266717;
 RA Walz D.A., Hewett-Emmett D., Seegers W.H.;
 RT "Amino acid sequence of human prothrombin fragments 1 and 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
 RN [4]
 RP SEQUENCE OF 315-622.
 RX MEDLINE=77207112; PubMed=673923;
 RA Burkowski R.J., Elton J., Downing M.R., Mann K.G.;
 RT "Primary structure of human prothrombin 2 and alpha-thrombin.";
 RL J. Biol. Chem. 252:4942-4957(1977).
 RN [5]
 RP PROCESSING.
 RX MEDLINE=87008532; PubMed=3759958;
 RA Rabiet M.J., Blashill A., Furie B., Furie B.C.;
 RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin
 activation in human plasma.";
 RL J. Biol. Chem. 261:13210-13215(1986).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=90059942; PubMed=2583108;
 RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;
 RT "The refined 1.9 A crystal structure of human alpha-thrombin:
 interaction with D-Phe-Pro-Arg chloromethylketone and significance of
 the Tyr-Pro-Pro-Tyr insertion segment.";
 RL EMBO J. 8:3467-3475(1989).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=90327074; PubMed=3374926;
 RA Rygel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
 RA Roltsch C., Fenton J.W. II;
 RT "The structure of a complex of recombinant hirudin and human alpha-
 thrombin.";
 RL Science 249:277-280(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94350942; PubMed=8071320;
 RA Rygel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,
 RA Correa P.E., Fenton J.W. II, Tulinsky A.;
 RT "Crystallographic structure of human gamma-thrombin.";
 RL J. Biol. Chem. 269:22000-22006(1994).

RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=97357286; PubMed=9214615;
 RA van de Loch A., Bode W., Huber R., le Bonniec B.F., Stone S.R.,
 RA Esmen C.T., Stubbs M.T.;
 RT "The thrombin E192Q-BPTI complex reveals gross structural
 rearrangements: implications for the interaction with antithrombin
 and thrombomodulin.";
 RL EMBO J. 16:2977-2984(1997).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
 RX MEDLINE=99162521; PubMed=10051558;
 RA Guinio E.R., Gacela S., Rose T., Fuellener K., Waksman G., di Cera E.;
 RT "Unexpected crucial role of residue 225 in serine proteases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
 RN [11]
 RP VARIANT BARCELONA.
 RX MEDLINE=87033739; PubMed=3771562;
 RA Rabiet M.-J., Furie B.C., Furie B.;
 RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine
 for arginine at residue 273.";
 RL J. Biol. Chem. 261:15045-15048(1986).
 RN [12]
 RP VARIANT FRANKFURT.
 RX MEDLINE=95313001; PubMed=7792730;
 RA Degen S.J.F., McDowell S.A., Sparks L.M., Scharer I.;
 RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by
 substitution of Glu-466 by Ala.";
 RL Thromb. Haemost. 73:203-209(1995).
 RN [13]
 RP VARIANTS HIMI-1 AND HIMI-2.
 RX MEDLINE=93043342; PubMed=1421398;
 RA Morishita E., Saico M., Kumabashiri I., Asakura H., Matsuda T.,
 RA Yamaguchi K.;
 RT "Prothrombin Himi: a compound heterozygote for two dysfunctional
 prothrombin molecules (Met-337->Thr and Arg-388->His).";
 RL Blood 80:2275-2280(1992).
 RN [14]
 RP VARIANT PADUA-1.
 RX MEDLINE=95169898; PubMed=7865694;
 RA James H.L., Kim D.-J., Zheng D.-Q., Girolami A.;
 RT "Prothrombin Padua I: incomplete activation due to an amino acid
 substitution at a factor Xa cleavage site.";
 RL Blood Coagul. Fibrinolysis 5:841-844(1994).
 RN [15]
 RP VARIANT QUICK-1.
 RX MEDLINE=89207504; PubMed=3242619;
 RA Henriksen R.A., Mann K.G.;
 RT "Identification of the primary structural defect in the dysprothrombin
 thrombin Quick I: substitution of cysteine for arginine-382.";
 RL Biochemistry 27:9160-9165(1988).
 RN [16]
 RP VARIANT QUICK-2.
 RX MEDLINE=89247398; PubMed=2719946;
 RA Henriksen R.A., Mann K.G.;
 RT "Substitution of valine for glycine-558 in the congenital dysprothrombin
 thrombin Quick II alters primary substrate specificity.";
 RL Biochemistry 28:2078-2082(1989).
 RN [17]
 RP VARIANT SALAKTA.
 RX MEDLINE=92378975; PubMed=1354985;
 RA Miyata T., Aruga R., Umeyama H., Bezeaud A., Guillan M.-C.,
 RA Iwanaga S.;
 RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine
 reduces the fibrinogen clotting activity and the esterase activity.";
 RL Biochemistry 31:7457-7462(1992).
 RN [18]
 RP VARIANT TOKUSHIMA.
 RX MEDLINE=87185407; PubMed=3567158;
 RA Miyata T., Morita T., Inomoto T., Kawachi S., Shirakami A.,
 RA Iwanaga S.;
 RT "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan
 that impairs the fibrinogen clotting activity of derived thrombin

RT Tokushima.*;
 RL Biochemistry 26:1117-1122(1987).
 RL [19]
 RP VARIANT TOKUSHIMA.
 RX MEDLINE-87101511; PubMed-3801671;
 RA Inamoto T., Shirakami A., Kawachi S., Shigekiyo T., Saito S.,
 RA Miyoshi K., Morita T., Iwanaga S.;
 RT "Prothrombin Tokushima: characterization of dysfunctional thrombin
 RT derived from a variant of human prothrombin.";
 RL Blood 69:565-569(1987).
 RN [20]
 RP VARIANT TOKUSHIMA.
 RX MEDLINE-92256895; PubMed-1349838;
 RA Iwawana H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito S.,
 RA Itakura M.;
 RT "Detection of a single base substitution of the gene for prothrombin
 RT Tokushima. The application of PCR-SSCP for the genetic and molecular
 RT analysis of dysprothrombinemia.";
 RL Int. J. Hematol. 55:93-100(1992).
 RN [21]
 RP VARIANT TYPE-3.
 RX MEDLINE-83204687; PubMed-6405779;
 RA Board P.G., Shaw D.C.;
 RT "Determination of the amino acid substitution in human prothrombin
 RT type 3 (157 Glu leads to Lys) and the localization of a third
 RT thrombin cleavage site.";
 RL Br. J. Haematol. 54:245-254(1983).
 CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOYAL
 CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CC OF PROTHROMBIN TO THROMBIN.
 CC -1- DISEASE: DEFECTS IN F2 ARE THE CAUSE OF VARIOUS FORMS OF
 CC DYSPROTHROMBINEMIA.
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 CC THROMBIN.
 CC -1- MISCELLANEOUS: IT IS NOT KNOWN WHETHER 1 OR 2 SMALLER ACTIVATION
 CC PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEASED IN
 CC NATURAL BLOOD CLOTTING.
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC -1- MISCELLANEOUS: THE CLEAVAGE AFTER R-198, OBSERVED IN VITRO, DOES
 CC NOT OCCUR IN PLASMA.
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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Query Match 51.4%; Score 71; DB 1; Length 622;
 Best local similarity 64.7%; Pred. No. 0.0099;

Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNPDSGTGFWAYTNP 17
 DB 158 RNPDSGTGFWAYTNP 174

RESULT 22
 APOA_MACMU

ID APOA_MACMU STANDARD; PRT; 1420 AA.
 AC P14417;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Apolipoprotein(a) (EC 3.4.21.-) (Apo(a)) (Lp(a)) (Fragment).
 GN LPA.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 CC NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89174660; PubMed-2925643;
 RA Tomlinson J.E., McLean J.W., Lawn R.M.;
 RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
 RT synthesis.";
 RL J. Biol. Chem. 264:5957-5965(1989).
 CC -1- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
 CC (Lp(a)). It has serine proteinase activity and is able of
 CC autolysis. It inhibits tissue-type plasminogen activator 1.
 CC Lp(a) may be a ligand for megalin/6p 330.
 CC -1- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
 CC decorin (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- DISEASE: Elevated plasma concentrations of apo(a) and its
 CC naturally occurring proteolytic fragments is correlated with
 CC atherosclerosis. Homology with plasminogen kringle IV and V is
 CC thought to underlie the atherogenicity of the protein, because the
 CC fragments are competing with plasminogen for fibrin(ogen) binding.
 CC -1- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
 CC leading to the formation of the so called mini-Lp(a). Apo(a)
 CC fragments accumulate in atherosclerotic lesions, where they may
 CC promote thrombogenesis. O-glycosylation may limit the extent of
 CC proteolytic fragmentation (By similarity).
 CC -1- SIMILARITY: CONTAINS AT LEAST 10 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
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 CC -----
 CC EMBL: J04635; AAA36833.1; -;
 CC PIR: A30848; A30848.
 CC PIR: A32869; A32869.
 CC HSSP: P00747; 2PK4.
 CC MEROPS: S01.226; -;
 CC InterPro: IPR000001; Kringle.
 CC InterPro: IPR001254; Trypsin.
 CC Pfam: PF00051; Kringle_10.
 CC Pfam: PF00089; trypsin_1.
 CC SMART: SM00130; KR_10.
 CC SMART: SM00020; TRYP_SPC_1.
 CC PROSITE: PS00021; KRINGLE_1; 9.
 CC PROSITE: PS00070; KRINGLE_2; 10.
 CC PROSITE: PS0240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
 CC PROSITE: PS00135; TRYPSIN_SER; FALSE_NEG.
 CC Hydroxylase: Serine protease; Lipid transport; Plasma; Glycoprotein;
 CC Kringle; Repeat; Atherosclerosis.
 CC K1 NON_TER 1
 CC FT DOMAIN 49 127 KRINGLE 1.
 CC FT DOMAIN 163 241 KRINGLE 2.
 CC FT DOMAIN 277 355 KRINGLE 3.
 CC FT DOMAIN 391 469 KRINGLE 4.
 CC FT DOMAIN 505 583 KRINGLE 5.
 CC FT DOMAIN 619 697 KRINGLE 6.

FT DOMAIN 725 803 KRINGLE 7.
 FT DOMAIN 839 917 KRINGLE 8.
 FT DOMAIN 953 1031 KRINGLE 9.
 FT DOMAIN 1067 1145 KRINGLE 10.
 FT DOMAIN 1191 1420 SERINE PROTEASE.
 SQ SEQUENCE 1420 AA; 158367 MW; BE102949E03C5B0E CRC64;

Query Match 47.5%; Score 65.5; DB 1; Length 1420;
 Best Local Similarity 47.8%; Pred. No. 0.15;
 Matches 11; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

OY 1 RNDGCVGGMWATTPNRKLYDY 23
 Db 776 RNDPAEI-RPWCYTMDFRVMEX 797

RESULT 23
 YE90_MYCTU STANDARD; PRT; 435 AA.
 AC P17171;

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypoetical 48.2 kDa protein Rv1490.
 GN Rv1490 OR MT1536 OR MTCY277.12.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_Taxid=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE=98293987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Bigniemel K., Gas S., Barry C.E. III, Tekaita F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,
 RA Horsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrall B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayan L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouli H., Gill J., Mikula A.,
 RA Bishai W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Laboratory (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC

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DR EMBL; Z79701; CAB02040.1; -
 DR EMBL; AE007022; AAK45803.1; -
 DR TIGR; MT1536; -
 DR TubercuList; Rv1490; -
 KM Hypoetical protein: Transmembrane; Complete proteome.
 FT TRANSMEM 40 60 POTENTIAL.
 FT TRANSMEM 103 123 POTENTIAL.
 FT TRANSMEM 133 153 POTENTIAL.

FT TRANSMEM 195 215 POTENTIAL.
 FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 313 333 POTENTIAL.
 FT TRANSMEM 358 378 POTENTIAL.
 FT TRANSMEM 381 401 POTENTIAL.
 FT TRANSMEM 414 434 POTENTIAL.
 SQ SEQUENCE 435 AA; 48149 MW; 1144B549CD418F30 CRC64;

Query Match 43.5%; Score 60; DB 1; Length 435;
 Best Local Similarity 47.6%; Pred. No. 0.27;
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 3 PGDVGGMWATTPNRKLYDY 23
 Db 259 PGHVENPWAATTPORVLDY 279

RESULT 24
 ROR2_HUMAN STANDARD; PRT; 943 AA.
 AC Q01974; Q9HAT7; Q9HB61;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tyrosine-protein kinase transmembrane receptor ROR2 precursor
 DE (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2).
 GN ROR2 OR NTRK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93100347; PubMed=1334494;
 RA Maslakowski P., Carroll R.D.;
 RT "A novel family of cell surface receptors with tyrosine kinase-like
 RL domain."
 RL J. Biol. Chem. 267:26181-26190(1992).
 RN [2]
 RP SEQUENCE OF 34-943 FROM N.A. AND VARIANT ILE-819.
 RX MEDLINE=20164326; PubMed=10700182;
 RA Oldridge M., Fortuna A.M., Maringa M., Propping P., Mansour S.,
 RA Pollitt C., DeChiara T.M., Kimble R.B., Valenzuela D.M.,
 RA Yancopoulos G.D., Wilkie A.O.M.;
 RT "Dominant mutations in ROR2, encoding an orphan receptor tyrosine
 RT kinase, cause brachydactyly type B."
 RL Nat. Genet. 24:275-278(2000).
 RN [3]
 RP SEQUENCE OF 34-574 FROM N.A. AND VARIANT THR-245.
 RX MEDLINE=20442029; PubMed=10966040;
 RA Schwabe G.C., Tinschert S., Buschow C., Meincke P., Wolff G.,
 RA Gillissen-Kaesbach G., Oldridge M., Wilkie A.O.M., Koeneke R.,
 RA Mundlos S.;
 RT "Distinct mutations in the receptor tyrosine kinase gene ROR2 cause
 RT brachydactyly type B."
 RL Am. J. Hum. Genet. 67:822-831(2000).
 RN [4]
 RP VARIANTS RRS C-184; W-189; W-366 AND K-620.
 RX MEDLINE=20392395; PubMed=10932187;
 RA Afzal A.R., Rajab A., Fenske C.D., Oldridge M., Elanko N.,
 RA Tenes-Pereira E., Tunesuez B., Murday V.A., Patton M.A.,
 RA Wilkie A.O.M., Jeffery S.;
 RT "Recessive Robinow syndrome, allelic to dominant brachydactyly type B,
 RT is caused by mutation of ROR2."
 RL Nat. Genet. 25:419-422(2000).
 RN [5]
 RP VARIANT RRS TYR-182.
 RX MEDLINE=20392395; PubMed=10932187;
 RA van Bokhoven H., Celli J., Kayserili H., van Beusekom E., Balci S.,
 RA Brussel M., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.G.;
 RT "Mutation of the gene encoding the ROR2 tyrosine kinase causes
 RL autosomal recessive Robinow syndrome."
 RL Nat. Genet. 25:423-426(2000).

[6]
 RA van Bokhoven H., Celli J., Kayserili H., van Bensekom E., Balci S.,
 RA Brussels W., Skovby F., Kerr B., Percin E.F., Akatsu N., Brunner H.G.,
 RL Nat. Genet. 26:383-383(2000).
 CC -1- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHICH MAY BE INVOLVED
 CC IN THE EARLY FORMATION OF THE CHONDROCYTES. IT SEEMS TO BE
 CC REQUIRED FOR CARTILAGE AND GROWTH PLATE DEVELOPMENT.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS DURING EARLY
 CC EMBRYONIC DEVELOPMENT. THE EXPRESSION LEVELS DROE STRONGLY AROUND
 CC DAY 16 AND THERE ARE ONLY VERY LOW LEVELS IN ADULT TISSUES.
 CC -1- DISEASE: DEFECTS IN ROR2 ARE A CAUSE OF BRACHYDACTYLITY TYPE B
 CC (BDB). BDB IS AN AUTOSOMAL DOMINANT SKELETAL DISORDER
 CC CHARACTERIZED BY HYPOPLASIA/APLASIA OF DISTAL PHALANGES AND NAILS.
 CC IN BDB THE MIDDLE PHALANGES ARE SHORT BUT IN ADDITION THE TERMINAL
 CC PHALANGES ARE REDUNDANTARY OR ABSENT. BOTH FINGERS AND TOES ARE
 CC AFFECTED. THE THUMBS AND BIG TOES ARE USUALLY DEFORMED.
 CC -1- DISEASE: DEFECTS IN ROR2 ARE A CAUSE OF RECESSIVE ROBINOW SYNDROME
 CC (RRS). RRS IS AN AUTOSOMAL DISORDER CHARACTERIZED BY SKELETAL
 CC DYSPLASIA WITH GENERALIZED LIMB BONE SHORTENING, SEGMENTAL DEFECTS
 CC OF THE SPINE, BRACHYDACTYLITY AND A DYSMORPHIC FACIAL APPEARANCE.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN, BELONGS TO THE ROR SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: M97639, AAA60276.1, -
 DR EMBL: AF294796; AAG01184.2, -
 DR EMBL: AF254747; AAG01184.2, JOINED.
 DR EMBL: AF254748; AAG01184.2, JOINED.
 DR EMBL: AF254749; AAG01184.2, JOINED.
 DR EMBL: AF254750; AAG01184.2, JOINED.
 DR EMBL: AF254751; AAG01184.2, JOINED.
 DR EMBL: AF254752; AAG01184.2, JOINED.
 DR EMBL: AF254753; AAG01184.2, JOINED.
 DR EMBL: AF279762; AAG3132.1, -
 DR EMBL: AF279765; AAG3132.1, JOINED.
 DR EMBL: AF279756; AAG3132.1, JOINED.
 DR EMBL: AF279757; AAG3132.1, JOINED.
 DR EMBL: AF279758; AAG3132.1, JOINED.
 DR EMBL: AF279759; AAG3132.1, JOINED.
 DR EMBL: AF279760; AAG3132.1, JOINED.
 DR EMBL: AF279761; AAG3132.1, JOINED.
 DR HSSP: P00747; 1KRN.
 DR MIM: 602337; -
 DR MIM: 113000; -
 DR MIM: 268310; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF01392; Fz, 1.
 DR Pfam: PF00047; Ig, 1.
 DR Pfam: PF00051; kringle, 1.
 DR Pfam: PF00069; pkinase, 1.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00408; IGC2, 1.
 DR SMART: SM00130; KR, 1.
 DR SMART: SM00219; TyKc, 1.

[illegible]

RX MEDLINE-99248426; PubMed-10231392;
 RA Oishi I., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.J.,
 RA Hata T., Akira S., Matsuda Y., Yamamura H., Ohtani H., Minami Y.,
 RT "Spatio-temporally regulated expression of receptor tyrosine kinases,
 RT mRor1, mRor2, during mouse development: implications in development
 RT and function of the nervous system.",
 RL Genes Cells 4:41-56(1999).
 RP CHARACTERIZATION.
 RX MEDLINE-20164325; PubMed-10700181;
 RA Dechiara T.M., Kimble R.B., Poneymirou W.T., Rojas J., Maslakowski P.,
 RA Valenzuela D.M., Yancopoulos G.D.,
 RT "Ror2, encoding a receptor-like tyrosine kinase, is required for
 RT cartilage and growth plate development.",
 RL Nat. Genet. 24:271-274(2000).
 CC -1- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHICH MAY BE INVOLVED
 CC IN THE EARLY FORMATION OF THE CHONDROCYTES. IT SEEMS TO BE
 CC REQUIRED FOR CARTILAGE AND GROWTH PLATE DEVELOPMENT.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (Fz) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE ROR SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; AB010384; BAA75481.1; -
 DR HSSP; P00747; 5HPG.
 DR MGD; MGI:1347521; Ror2.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR00109; TYRKINASE.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00219; TYKC; 1.
 DR PROSITE; PS50038; Fz; 1.
 DR PROSITE; PS00021; KRINGLE_1; FALSE_NEG.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Receptor;
 KW Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
 KW Immunoglobulin domain; Developmental protein.
 FT SIGNAL 1
 FT CHAIN 34
 FT CHAIN 944
 FT DOMAIN 34
 FT DOMAIN 403
 FT TRANSMEM 404
 FT TRANSMEM 424
 FT DOMAIN 425
 FT DOMAIN 444
 FT DOMAIN 469
 FT DOMAIN 303
 FT DOMAIN 316
 FT DOMAIN 394
 FT DOMAIN 473
 FT DOMAIN 746
 FT DOMAIN 753
 FT DOMAIN 782
 FT SER/THR-RICH.

FT DOMAIN 784 857 PRO-RICH.
 FT DOMAIN 859 882 SER/THR-RICH.
 FT NP_BIND 479 487 ATP (BY SIMILARITY).
 FT BINDING 507 507 ATP (BY SIMILARITY).
 FT ACT_SITE 615 615 BY SIMILARITY.
 FT MOD_RES 646 646 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT DISULFID 83 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 70 70 CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 944 AA; 105050 MW; CD2EEBC710387A56 CRC64.
 Query Match 42.8%; Score 59; DB 1; Length 944;
 Best Local Similarity 56.2%; Pred. No. 0.83;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Db 366 RNPQGVGGPWATYTN 16
 1 RNPQGVGGPWATYTN 16
 ||| | : ||| : |
 Db 366 RNPQGVGGPWATYTN 16
 RESULT 26
 TPA_MOUSE
 ID TPA_MOUSE STANDARD; PRT; 559 AA.
 AC P11214;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (TPA)
 DE (t-PA) (t-plasminogen activator).
 GN PLAT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88087303; PubMed-2826484;
 RA Rickles R.J., Darrow A.L., Strickland S.;
 RT "Molecular cloning of complementary DNA to mouse tissue plasminogen
 RT activator mRNA and its expression during F9 teratocarcinoma cell
 RT differentiation.",
 RL J. Biol. Chem. 263:1563-1569(1988).
 CC -1- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN
 CC TO PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN. BY
 CC CONTROLLING PLASMIN-MEDIATED PROTEOLYSIS, IT PLAYS AN IMPORTANT
 CC ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND
 CC MANY OTHER PHYSIOPATHOLOGICAL EVENTS.
 CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 CC plasminogen to form plasmin.
 CC -1- SUBUNIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
 CC BOND.
 CC -1- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.
 CC -1- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER
 CC PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER
 CC ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
 CC -1- MISCELLANEOUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A
 CC CHAIN. BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE I DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; J03520; AAA0470.1; -

DR PIR; A29941; A29941.
 DR HSSP; P00750; 1TPG.
 DR MEROPS; S01.232; -
 DR MGD; MGI:97610; Plat.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Trypsin.
 DR InterPro; IPR000083; fibronectin_type_1.
 DR Pfam; PF00008; EGF_1.
 DR Pfam; PF00039; Fnl_1.
 DR Pfam; PF00051; kringle_2.
 DR Pfam; PF00089; trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00181; EGF_1.
 DR SMART; SM00058; Fnl_1.
 DR SMART; SM00130; KR_2.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS50070; KRINGLE_2; 2.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 KW Plasmidogen activation; Hydrolase; Serine protease; Glycoprotein;
 KM Plasma; Kringle; EGF-like domain; Signal.
 FT SIGNAL; 1 17 PROBABLE.
 FT PROPEP 18 29 TISSUE-TYPE PLASMINOGEN ACTIVATOR.
 FT CHAIN 30 559 TISSUE-TYPE PLASMINOGEN ACTIVATOR A
 FT CHAIN 30 308 CHAIN.
 FT CHAIN 309 559 TISSUE-TYPE PLASMINOGEN ACTIVATOR B
 FT CHAIN.
 FT DOMAIN 36 78 FIBRONECTIN TYPE-1.
 FT DOMAIN 79 117 EGF-LIKE.
 FT DOMAIN 124 205 KRINGLE_1.
 FT DOMAIN 213 294 KRINGLE_2.
 FT DOMAIN 309 559 SERINE PROTEASE.
 FT ACT_SITE 355 355 CHARGE RELAY SYSTEM.
 FT ACT_SITE 404 404 CHARGE RELAY SYSTEM.
 FT ACT_SITE 510 510 CHARGE RELAY SYSTEM.
 FT DISULFID 38 68 BY SIMILARITY.
 FT DISULFID 66 75 BY SIMILARITY.
 FT DISULFID 83 94 BY SIMILARITY.
 FT DISULFID 88 105 BY SIMILARITY.
 FT DISULFID 107 116 BY SIMILARITY.
 FT DISULFID 124 205 BY SIMILARITY.
 FT DISULFID 145 187 BY SIMILARITY.
 FT DISULFID 176 200 BY SIMILARITY.
 FT DISULFID 213 294 BY SIMILARITY.
 FT DISULFID 234 276 BY SIMILARITY.
 FT DISULFID 265 289 BY SIMILARITY.
 FT DISULFID 297 428 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 340 356 BY SIMILARITY.
 FT DISULFID 348 417 BY SIMILARITY.
 FT DISULFID 442 516 BY SIMILARITY.
 FT DISULFID 474 490 BY SIMILARITY.
 FT DISULFID 506 534 BY SIMILARITY.
 FT CARBOHYD 149 149 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC...) (POTENTIAL).
 SO SEQUENCE 559 AA; 63110 MW; 4ACE57DC6A282A5 CRC64;

Query Match 40.6%; Score 56; DB 1; Length 559;
 Best Local Similarity 50.0%; Pred. No. 1.3;
 Matches 12; Conservative 3; Mismatches 7; Indels 2; Gaps 2;

QY 1 RNPDGVCWFAYTTPNRKL-YDY 23
 ||||| | : ||| : :
 DB 266 RNPDGD-ARPCWCMKDKRLTWEX 288

RESULT 27
 ID TPA_RAT STANDARD: PRT: 559 AA.
 AC P19637;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tissue-type plasminogen activator precursor (BC 3.4.21.68) (tPA)
 DE (t-PA) (t-plasminogen activator).
 GN PLAT.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89170114; PubMed=3148445;
 RA Ny T., Leonardsson G., Hsueh A.J.W.;
 RT "Cloning and characterization of a cDNA for rat tissue-type
 RL plasminogen activator."
 RL DNA 7:671-677(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90130448; PubMed=2105315;
 RA Feng P., Ohlsson M., Ny T.;
 RT "The structure of the tPA-less rat tissue-type plasminogen activator
 RT gene. Species-specific sequence divergences in the promoter predict
 RT differences in regulation of gene expression."
 RL J. Biol. Chem. 265:2022-2027(1990).
 CC -1- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZMOGEN PLASMINOGEN
 CC TO PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN. BY
 CC CONTROLLING PLASMIN-MEDIATED PROTEOLYSIS, IT PLAYS AN IMPORTANT
 CC ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND
 CC MANY OTHER PHYSIOLOGICAL EVENTS.
 CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-1-val bond in
 CC plasminogen to form plasmin.
 CC -1- SUBUNIT: HETERO DIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
 CC BOND.
 CC -1- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.
 CC -1- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER
 CC PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER
 CC ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
 CC -1- MISCELLANEOUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A
 CC CHAIN. BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE I DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPsin FAMILY.
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 CC -----
 DR EMBL; M23697; AAA41812.1; -;
 DR EMBL; M31197; AAA42261.1; -;
 DR EMBL; M31185; AAA42261.1; JOINED.
 DR EMBL; M31186; AAA42261.1; JOINED.
 DR EMBL; M31187; AAA42261.1; JOINED.
 DR EMBL; M31188; AAA42261.1; JOINED.
 DR EMBL; M31189; AAA42261.1; JOINED.
 DR EMBL; M31190; AAA42261.1; JOINED.
 DR EMBL; M31191; AAA42261.1; JOINED.
 DR EMBL; M31192; AAA42261.1; JOINED.
 DR EMBL; M31193; AAA42261.1; JOINED.
 DR EMBL; M31194; AAA42261.1; JOINED.
 DR EMBL; M31195; AAA42261.1; JOINED.
 DR EMBL; M31196; AAA42261.1; JOINED.


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QY      1  RNPDDGVGGPWAYTTNPKKL-YDY  23
      |||||  ||  |||  ::|

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DB      266  RNPDBG-AKPMCHVMKDRKLTWEY 288

RESULT 28
PHLN_BURPS
AC      Q9RGS8;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Non-hemolytic phospholipase C precursor (EC 3.1.4.3) (PLC-N)
DE      (Phosphatidylcholine cholinephosphohydrolase) (Phosphatidylcholine-
GN      hydrolyzing phospholipase C) (PC-PLC).
OS      Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC      Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC      Burkholderia.
OX      NCBI_TaxID=28450;
RN      [1]
RP      SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC      STRAIN-SPTL;
RX      MEDLINE=99454884; PubMed=10523590;
RA      Korbestrate S., Suwanasai N., Leelaporn A., Ezaki T., Kawamura Y.,
RA      Sarasombath S.;
RT      "Cloning and characterization of a nonhemolytic phospholipase C gene
RT      from Burkholderia pseudomallei."
RL      J. Clin. Microbiol. 37:3742-3745(1999).
CC      -1- FUNCTION: HYDROLYZES PHOSPHATIDYLERINE AS WELL AS
CC      PHOSPHATIDYCHOLINE.
CC      -1- CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)O = 1,2-
CC      diacylglycerol + choline phosphate.
CC      -1- SIMILARITY: BELONGS TO THE BACTERIAL PHOSPHOLIPASE C FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF107252; AAF17299.1; -.
DC      KW      Hydrolase; Signal.
FT      SIGNAL      1      19      POTENTIAL.
FT      CHAIN      20      700      NON-HEMOLYTIC PHOSPHOLIPASE C.
SQ      SEQUENCE      700 AA; 77190 MW; 5EDA66FCDFB129B CRC64;

Query March      38.0%; Score 52.5; DB 1; Length 700;
Best local Similarity 41.4%; Pred. NO. 5.3;
Matches 12; Conservative 0; Mismatches 4; Indels 13; Gaps 1;

QY      7      VGGPMAYTTNPRK-----LYD 22
                1 111111 11
                548 VDGPMAYTVEARKRISDEWSTALTLISYD 576
                1 111111 11

RESULT 29
TPA_HUMAN
ID      TPA_HUMAN      STANDARD;      PRT;      562 AA.
AC      P00750; Q15103;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
DE      (t-PA) (t-plasminogen activator) (Alteplase) (Releplase).
GN      PLAT.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Melanoma;

```

- RA MEDLINE=83115262; PubMed=6337343;
RA Pennica D., Holmes W.E., Kohr W.J., Harkins R.N., Vehar G.A.,
RA Ward C.A., Bennett W.F., Yelverton E., Seeburg P.H., Heyneker H.L.,
RA Goeddel D.V., Collen D.;
RT "Cloning and expression of human tissue-type plasminogen activator
RT cDNA in E. coli.";
RL Nature 301:214-221(1983).
RN
RP
RC TISSUE-Fetal lung; PubMed=3133640;
RX MEDLINE=88262579; PubMed=3133640;
RA Sasaki H., Saito Y., Hayashi M., Otsuka K., Miwa M.;
RT "Nucleotide sequence of the tissue-type plasminogen activator cDNA
RT from human fetal lung cells.";
RL Nucleic Acids Res. 16:5695-5695(1988).
RN
RP
RX SEQUENCE FROM N.A.
RX MEDLINE=88054470; PubMed=2824147;
RA Reddy V.B., Garramone A.J., Sasak H., Wei C.-M., Watkins P., Gall J.,
RA Hsing N.;
RT "Expression of human uterine tissue-type plasminogen activator in
RT mouse cells using BPV vectors.";
RL DNA 6:461-472(1987).
RN
RP
RX SEQUENCE FROM N.A.
RX MEDLINE=86196143; PubMed=3009482;
RA Friezner Degen S.J., Rajput B., Reich E.;
RT "The human tissue plasminogen activator gene";
RL J. Biol. Chem. 261:6972-6985(1986).
RN
RP
RX SEQUENCE FROM N.A.
RX MEDLINE=84298137; PubMed=6089198;
RA Ny T., Elgh F., Lund B.;
RT "The structure of the human tissue-type plasminogen activator gene:
RT correlation of intron and exon structures to functional and
RT structural domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5355-5359(1984).
RN
RP
RX SEQUENCE FROM N.A.
RX MEDLINE=86284200; PubMed=3090401;
RA Harris T.J., Patel T., Marston F.A., Little S., Emtage J.S.,
RA Opendakker G., Volckaert G., Rombaux W., Billiau A., Somer P.;
RT "Cloning of cDNA coding for human tissue-type plasminogen activator
RT and its expression in Escherichia coli.";
RL Mol. Biol. Med. 3:279-292(1986).
RN
RP
RX SEQUENCE OF 212-361 FROM N.A.
RX MEDLINE=83169656; PubMed=6572897;
RA Edlund T., Ny T., Raanby M., Heden L.-O., Palm G., Holmgren E.,
RA Josephson S.;
RT "Isolation of cDNA sequences coding for a part of human tissue
RT plasminogen activator";
RL Proc. Natl. Acad. Sci. U.S.A. 80:349-352(1983).
RN
RP
RX SEQUENCE OF 1-36 FROM N.A.
RX MEDLINE=85289338; PubMed=3161893;
RA Fisher R., Waller E.K., Grossi G., Thompson D., Tizard R.,
RA Schleming W.-D.;
RT "Isolation and characterization of the human tissue-type plasminogen
RT activator structural gene including its 5' flanking region.";
RL J. Biol. Chem. 260:11223-11230(1985).
RN
RP
RX SEQUENCE OF 31-562 FROM N.A.
RX MEDLINE=91291340; PubMed=1368681;
RA Itagaki Y., Yasuda H., Morinaga T., Mitsuda S., Higashio K.;
RT "Purification and characterization of tissue plasminogen activator
RT secreted by human embryonic lung diploid fibroblasts, IMR-90 cells.";
RL Agric. Biol. Chem. 55:1225-1232(1991).
RN
RP
RX SPOURCE OF 36-562.
RX TISSUE-Melanoma;
RX MEDLINE=85000468; PubMed=6433976;
RA Pohl G., Kaellstroem M., Bergsdorf N., Wallen P., Joernvall H.;
- RT "Tissue plasminogen activator: peptide analyses confirm an indirectly
RT derived amino acid sequence, identify the active site serine residue,
RT establish glycosylation sites, and localize variant differences.";
RL Biochemistry 23:3701-3707(1984).
RN
RP
RX SEQUENCE OF 33-52 AND 311-330.
RX TISSUE-Melanoma;
RX MEDLINE=83209620; PubMed=6682760;
RA Wallen P., Pohl G., Bergsdorf N., Raanby M., Ny T., Joernvall H.;
RT "Purification and characterization of a melanoma cell plasminogen
RT activator.";
RL Eur. J. Biochem. 132:681-686(1983).
RN
RP
RX SEQUENCE FROM N.A. (SHORT ISOFORM).
RX TISSUE-Umbilical vein;
RX MEDLINE=90192129; PubMed=2107528;
RA Siebert P.D., Fong K.;
RT "Variant tissue-type plasminogen activator (PLAT) cDNA obtained from
RT human endothelial cells.";
RL Nucleic Acids Res. 18:1086-1086(1990).
RN
RP
RX STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=90092112; PubMed=2513186;
RA Pfeiffer G., Schmidt M., Strube K.-H., Geyer R.;
RT "Carbohydrate structure of recombinant human uterine tissue
RT plasminogen activator expressed in mouse epithelial cells.";
RL Eur. J. Biochem. 186:273-286(1989).
RN
RP
RX CARBOHYDRATE-LINKAGE SITE THR-96.
RX MEDLINE=91159408; PubMed=1900431;
RA Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.;
RT "Tissue plasminogen activator has an O-linked fucose attached to
RT threonine-61 in the epidermal growth factor domain.";
RL Biochemistry 30:2311-2314(1991).
RN
RP
RX DISULFIDE BONDS IN KRINGLE 2.
RX MEDLINE=91244765; PubMed=1645336;
RA Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.;
RT "Disulfide pairing of the recombinant kringle-2 domain of tissue
RT plasminogen activator produced in Escherichia coli.";
RL J. Biol. Chem. 266:10070-10072(1991).
RN
RP
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF CATALYTIC DOMAIN.
RX MEDLINE=96200983; PubMed=8613982;
RA Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
RA Bode W.;
RT "The 2.3 A crystal structure of the catalytic domain of recombinant
RT two-chain human tissue-type plasminogen activator";
RL J. Mol. Biol. 258:117-135(1996).
RN
RP
RX X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF CATALYTIC DOMAIN.
RX MEDLINE=97449126; PubMed=9305622;
RA Renatus M., Engh R.A., Stubbs M.T., Huber R., Fischer S., Kohnert U.,
RA Bode W.;
RT "Lysine 156 promotes the anomalous proenzyme activity of tPA: X-ray
RT crystal structure of single-chain human tPA";
RL EMBO J. 16:4797-4805(1997).
RN
RP
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2.
RX MEDLINE=92118803; PubMed=1310033;
RA de Vos A., Ullrich M.H., Kelley R.F., Pedmanabhan K., Tulinsky A.,
RA Westbroek M.L., Kossiakof A.A.;
RT "Crystal structure of the kringle 2 domain of tissue plasminogen
RT activator at 2.4-A resolution.";
RL Biochemistry 31:270-279(1992).
RN
RP
RX STRUCTURE BY NMR OF KRINGLE 2.
RX MEDLINE=90122799; PubMed=2556718;
RA Byeon I.-J.L., Kelley R.F., Linas M.;
RT "1H NMR structural characterization of a recombinant kringle 2 domain
RT from human tissue-type plasminogen activator.";
RL Biochemistry 28:9350-9360(1989).
RN

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RP STRUCTURE BY NMR OF KRINGLE 2.
RX MEDLINE=91200042; Pubmed=1901789;
RA Byeon I.-J.L., Kelley R.F., Llinas M.;
RT "Kringles-2 domain of the tissue-type plasminogen activator. 1H-NMR
RL assignments and secondary structure."
RU Eur. J. Biochem. 197;155-165(1991).
RN [21]
RP STRUCTURE BY NMR OF KRINGLE 2.
RX MEDLINE=91206329; Pubmed=1762144;
RA Byeon I.-J.L., Llinas M.;
RT "Solution structure of the tissue-type plasminogen activator kringle
RT 2 domain complexed to 6-aminohexanoic acid an antifibrinolytic
RT drug."
RL J. Mol. Biol. 222;1035-1051(1991).
RN [22]
RP STRUCTURE BY NMR OF 38-85.
RX MEDLINE=92292163; Pubmed=1602484;
RA Downing A.K., Driscoll P.C., Harvey T.S., Dudgeon T.J., Smith B.O.,
RT Baron M., Campbell I.D.;
RT "Solution structure of the fibrin binding finger domain of
RT tissue-type plasminogen activator determined by 1H nuclear magnetic
RT resonance."
RL J. Mol. Biol. 225;821-833(1992).
RN [23]
RP STRUCTURE BY NMR OF 36-126.
RX MEDLINE=96027104; Pubmed=7582899;
RA Smith B.O., Downing A.K., Driscoll P.C., Dudgeon T.J., Campbell I.D.;
RT "The solution structure and backbone dynamics of the fibronectin type
RT I and epidermal growth factor-like pair of modules of tissue-type
RT plasminogen activator."
RL Structure 3;823-833(1995).
CC -1- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN
CC TO PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN. BY
CC CONTROLLING PLASMIN-MEDIATED PROTEOLYSIS, IT PLAYS AN IMPORTANT
CC ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND
CC MANY OTHER PHYSIOPATHOLOGICAL EVENTS.
CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-1-Val bond in
CC plasminogen to form plasmin.
CC -1- SUBUNIT: BINDS TO FIBRIN WITH HIGH AFFINITY. THIS INTERACTION
CC
Query Match 37.7%; Score 52; DB 1; Length 562;
Best Local Similarity 45.8%; Pred. No. 5;
Matches 11; Conservative 4; Mismatches 7; Indels 2; Gaps 2;
OY 1 RNPDVGCPWATYNNPKRL-YDY 23
DB 268 RNPDDGD-ARPCWCHVLKRNRLTWEX 290

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RL Submitted (JUL-1993) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: TO A RHIZOGENES PLASMIND PRI4B ORF-3 IN VIRA REGION.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC
DR EMBL: X74068; CAA52198.1; ALT-INT.
DR EMBL: AE000077; AAB92455.1; -.
KW Hypothetical protein; Plasmin.
FT CONFLICT 18 18 I -> M (IN REF. 2).
FT CONFLICT 30 30 R -> S (IN REF. 2).
SQ SEQUENCE 194 AA; 21747 MW; 647B7161AF1513E3 CAC64;
Query Match 37.0%; Score 51; DB 1; Length 194;
Best Local Similarity 72.7%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 3 PDGVDGCPWAY 13
DB 128 PREDVGGPMGY 138

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RESULT 31
EST1_SCHGA STANDARD; PRT; 198 AA.
ID EST1_SCHGA
AC P81429;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Esterase SGI precursor (EC 3.1.1.1) (Carboxyl-ester hydrolase)
DE (Fragment).
DE SGI.
GN Schizaphis graminum (Aphid).
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
OC Aphidiformes; Aphidoidea; Aphididae; Aphidini; Schizaphis.
OX NCB1_TaxID=13262;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 22-41.
RX MEDLINE=20078165; Pubmed=10612041;
RA Ono M., Swanson J.J., Field L.M., Devonshire A.L., Siegfried B.D.;
RT "Amplification and methylation of an esterase gene associated with
RT insecticide-resistance in greenbugs, Schizaphis graminum."
RL Insect Biochem. Mol. Biol. 29;1065-1073(1999).
CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- MISCELLANEOUS: THIS ESTERASE CONFERS OP INSECTICIDE RESISTANCE.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC
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CC
DR EMBL: Y17580; CAA76792.1; -.
DR HSP: P37967; I0E3.
DR InterPro: IPR002018; Carboxylesterase_B.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 >198 ESTERASE SGI.

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FT DISULFID 87 104 BY SIMILARITY.
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 24 24 A -> T (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 28 28 R -> N (IN REF. 1; AA SEQUENCE).
 FT NON_TER 198 198
 SQ SEQUENCE 198 AA; 21897 MW; EFFE43EA6A5D5987 CRC64.
 Query Match 37.0%; Score 51; DB 1; Length 198;
 Best Local Similarity 42.1%; Pred. No. 2.3;
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 OY 5 GDVGGPWATTTNPKRLDY 23
 DB 32 GDVGGPWATTTNPKRLDY 50
 RESULT 32
 ESTE_MYZPE STANDARD; PRT; 552 AA.
 ID ESTE_MYZPE
 AC P35501;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Esterase E4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase).
 OS Myzus persicae (Peach-potato aphid).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
 OC Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus.
 OX NCBI_TaxID=13164;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-63.
 RC STRAIN=K3 / ISOLATE 794UJ;
 RX MEDLINE=93384534; PubMed=8373371;
 RA Field L.M., Williamson M.S., Moores G.D., Devonshire A.L.;
 RT "Cloning and analysis of the esterase genes conferring insecticide
 resistance in the peach-potato aphid, Myzus persicae (Sulzer).";
 RL Biochem. J. 294:569-574(1993).
 CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
 MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 carboxylic anion.
 CC -1- MISCELLANEOUS: THIS ESTERASE CONFERS INSECTICIDE RESISTANCE.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: X74554; CAA52648.1; -;
 DR PIR: S36786; S36786.
 DR HSSP: P21836; IMAH.
 DR InterPro: IPR002018; Carboxylesterase-B.
 DR InterPro: IPR000379; Est_lip_thioest_actsite.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; FALSE NEG.
 KW Hydrolyase; Serine esterase; Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 552
 FT ACT_SITE 214 552 ESTERASE E4.
 FT ACT_SITE 214 552 BY SIMILARITY.
 FT ACT_SITE 339 339 BY SIMILARITY.
 FT ACT_SITE 463 463 BY SIMILARITY.
 FT DISULFID 89 106 BY SIMILARITY.
 FT DISULFID 266 277 BY SIMILARITY.
 FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 552 AA; 61348 MW; B97B67272DFE7209 CRC64;
 Query Match 37.0%; Score 51; DB 1; Length 552;
 Best Local Similarity 42.1%; Pred. No. 6.8;
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 OY 5 GDVGGPWATTTNPKRLDY 23
 DB 34 GDVGGPWATTTNPKRLDY 52
 RESULT 33
 ESTE_MYZPE STANDARD; PRT; 564 AA.
 ID ESTE_MYZPE
 AC P35502;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Esterase E4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase).
 OS Myzus persicae (Peach-potato aphid).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
 OC Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus.
 OX NCBI_TaxID=13164;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-63.
 RC STRAIN=ISOLATE 800F;
 RX MEDLINE=93384534; PubMed=8373371;
 RA Field L.M., Williamson M.S., Moores G.D., Devonshire A.L.;
 RT "Cloning and analysis of the esterase genes conferring insecticide
 resistance in the peach-potato aphid, Myzus persicae (Sulzer).";
 RL Biochem. J. 294:569-574(1993).
 CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
 MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 carboxylic anion.
 CC -1- MISCELLANEOUS: THIS ESTERASE CONFERS INSECTICIDE RESISTANCE.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X74555; CAA52649.1; -;
 DR PIR: S36787; S36787.
 DR HSSP: P21836; IMAH.
 DR InterPro: IPR002018; Carboxylesterase-B.
 DR InterPro: IPR000379; Est_lip_thioest_actsite.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B.1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B.2; FALSE NEG.
 KW Hydrolyase; Serine esterase; Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 564
 FT ACT_SITE 214 564 ESTERASE E4.
 FT ACT_SITE 214 564 BY SIMILARITY.
 FT ACT_SITE 339 339 BY SIMILARITY.
 FT ACT_SITE 463 463 BY SIMILARITY.
 FT DISULFID 89 106 BY SIMILARITY.
 FT DISULFID 266 277 BY SIMILARITY.
 FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 564 AA; 62757 MW; 128CC0E3F2D9F1A CRC64;
 Query Match 37.0%; Score 51; DB 1; Length 564;
 Best Local Similarity 42.1%; Pred. No. 6.9;
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 5 GDVGGPWAYTTNPKLYD 23
 ID 34 GEIAGGFETYNKRIKISF 52

RESULT 34
 ID TPA_BOVIN STANDARD: PRT: 566 AA.

AC Q28198;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
 GN PLAT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Kidney;
 RT Ravn P., Berglund L., Petersen T.E.;
 RT and tPA.";
 RT "Cloning and characterization of the bovine plasminogen activators uPA
 and tPA.";
 RL Int. Dairy J. 5:605-617(1995).
 CC -1- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN
 TO PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN. BY
 CONTROLLING PLASMIN-MEDIATED PROTEOLYSIS, IT PLAYS AN IMPORTANT
 ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND
 MANY OTHER PHYSIOPATHOLOGICAL EVENTS.
 CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-Val bond in
 plasminogen to form plasmin.
 CC -1- SUBUNIT: HETERODIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
 BOND.
 CC -1- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.
 CC -1- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER
 PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER
 ARG-314 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
 CC -1- MISCELLANEOUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A
 CHAIN. BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE 1 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
 TRYPSIN FAMILY.

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 CC EMBL: X85800; CA59795.1; -
 CC HSSP: P00750; IRTF.
 CC DR HSSP: P00750; IRTF.
 DR MEROPS: S01.232; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000083; fibronectin_type_1.
 DR Pfam: PF00008; EGF_1.
 DR Pfam: PF00039; fn1; 1.
 DR Pfam: PF00051; kringle; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR SMART: SM00181; EGF; 1.
 DR SMART: SM00058; FN1; 1.
 DR SMART: SM00058; FN1; 1.

DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; TRYP-Spec; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 2.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasma; Kringle; EGF-like domain; Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 33
 FT CHAIN 34 566
 FT CHAIN 34 314
 FT CHAIN 315 566
 FT CHAIN 315 566
 FT DOMAIN 40 82
 FT DOMAIN 83 121
 FT DOMAIN 128 209
 FT DOMAIN 219 300
 FT DOMAIN 315 566
 FT ACT_SITE 361 361
 FT ACT_SITE 410 410
 FT ACT_SITE 517 517
 FT ACT_SITE 517 517
 FT DISULFID 42 72
 FT DISULFID 70 79
 FT DISULFID 87 98
 FT DISULFID 92 109
 FT DISULFID 111 120
 FT DISULFID 128 209
 FT DISULFID 149 191
 FT DISULFID 180 204
 FT DISULFID 219 300
 FT DISULFID 240 282
 FT DISULFID 271 295
 FT DISULFID 303 434
 FT DISULFID 346 362
 FT DISULFID 354 423
 FT DISULFID 448 523
 FT DISULFID 480 496
 FT DISULFID 513 541
 FT CARBOHYD 153 153
 FT CARBOHYD 487 487
 FT SEQUENCE 566 AA; 63701 MW; 2EB6BE4E32276C3 CRC64;

Query Match 37.0%; Score 51; DB 1; Length 566;
 Best Local Similarity 45.8%; Pred. No. 7;
 Matches 11; Conservative 4; Mismatches 7; Indels 2; Gaps 2;

OY 1 RNPDGWGPWAYTTNPKLT-YDY 23
 ID 272 RNPDGWGPWAYTTNPKLT-YDY 23

RESULT 35
 ID URTG_DESRO STANDARD: PRT: 394 AA.

AC P49150;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA
 gamma).
 OS Desmodus rotundus (Vampire bat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
 OC Desmodontinae; Desmodus.
 OX NCBI_TaxID=9430;
 RN [1]
 RP SEQUENCE FROM N.A.

CC TISSUE-Salivary gland.
 RX MEDLINE=92039036; PubMed=1937019;
 RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 RA Alagon A., Donner P., Schleuning W.D.;
 RT "The plasminogen activator family from the salivary gland of the
 RT vampire bat *Desmodus rotundus*: cloning and expression.";
 RL Gene 105:229-237(1991).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=93393059; PubMed=1309059;
 RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
 RA Kraetzschmar J., Haendler B., Langer G., Baldus B., Wilt W.,
 RA Donner P.;
 RT "Plasminogen activators from the saliva of *Desmodus rotundus* (common
 RT vampire bat): unique fibrin specificity.";
 RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
 CC -1- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS
 CC EXCLUSIVELY HAEMOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
 CC AGENT.
 CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 CC plasminogen to form plasmin.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 DR EMBL; M63990; AAA31595.1; -;
 DR HESP; P98119; 1A51.
 DR MEROPS; S01.239; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam; PF00051; Kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; TRYP-Spec; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Plasminogen activation; Hydrolyase; Serine protease; Glycoprotein;
 KW Kringle; Signal; Multigene family.
 FT SIGNAL 1 36
 FT CHAIN 37 394
 FT DOMAIN 45 126
 FT ACT_SITE 142 394
 FT ACT_SITE 189 189
 FT ACT_SITE 238 238
 FT ACT_SITE 345 345
 FT DISULFID 45 126
 FT DISULFID 66 108
 FT DISULFID 97 121
 FT DISULFID 131 262
 FT DISULFID 174 190
 FT DISULFID 182 251
 FT DISULFID 276 351
 FT DISULFID 308 324
 FT DISULFID 341 369
 FT CARBOHYD 315 315
 SQ SEQUENCE 394 AA: 44105 MW: 96CD6F52FDB81FCD CRC64;
 Query Match 36.6%; Score 50.5; DB 1; Length 394;

Best Local Similarity 52.6%; Pred. No. 5.6;
 Matches 10; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
 Qy 1 RNPDDGCGPMATYTNPK 19
 Db 98 RNPDC-ASKPCYVIRK 115
 RESULT 36
 FA12_HUMAN STANDARD; PRT; 615 AA.
 ID P00748; P78339;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
 DE (HAF).
 DE F12.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88007593; PubMed=2888762;
 RA Cool D.E., McGilivray R.T.A.;
 RT "Characterization of the human blood coagulation factor XII gene.
 RT Intron/exon gene organization and analysis of the 5'-flanking
 RT region.";
 RL J. Biol. Chem. 262:13662-13673(1987).
 RN [2]
 RP SEQUENCE OF 4-615 FROM N.A.
 RX MEDLINE=8616794; PubMed=3754331;
 RA Tripodi M., Citarella F., Guida S., Galeffi P., Fantoni A.,
 RA Cortese R.;
 RT "cDNA sequence coding for human coagulation factor XII (Hageman).";
 RL Nucleic Acids Res. 14:3146-3146(1986).
 RN [3]
 RP SEQUENCE OF 14-615 FROM N.A.
 RX MEDLINE=86033830; PubMed=3877053;
 RA Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.D.,
 RA McGilivray R.T.A.;
 RT "Characterization of human blood coagulation factor XII cDNA.
 RT Prediction of the primary structure of factor XII and the tertiary
 RT structure of beta-factor XIIa.";
 RL J. Biol. Chem. 260:13666-13676(1985).
 RN [4]
 RP SEQUENCE OF 146-615 FROM N.A.
 RX MEDLINE=86216049; PubMed=3011063;
 RA Que B.G., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor XII (Hageman
 RT factor).";
 RL Biochemistry 25:1525-1528(1986).
 RN [5]
 RP SEQUENCE OF 20-379.
 RX MEDLINE=85182674; PubMed=3886654;
 RA McMullen B.A., Fujikawa K.;
 RT "Amino acid sequence of the heavy chain of human alpha-factor XIIa
 RT (activated Hageman factor).";
 RL J. Biol. Chem. 260:5328-5341(1985).
 RN [6]
 RP SEQUENCE OF 354-362 AND 373-615.
 RX MEDLINE=83291041; PubMed=6604055;
 RA Fujikawa K., McMullen B.A.;
 RT "Amino acid sequence of human beta-factor XIIa.";
 RL J. Biol. Chem. 258:10924-10933(1983).
 RN [7]
 RP SEQUENCE OF 561-615 FROM N.A.
 RX MEDLINE=96133302; PubMed=8528215;
 RA Schloesser M., Hofferbert S., Bartz U., Lutze G., Jammle B., Engel W.;
 RT "The novel acceptor splice site mutation 11396(G->A) in the factor
 RT XII gene causes a truncated transcript in cross-reacting material

RT negative patients.";
 RL Hum. Mol. Genet. 4:1235-1237(1995).
 RN [8]
 RP VARIANT WASHINGTON DC.
 RX MEDLINE-90046788; PubMed-2510163;
 RA Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving B.,
 RT Saito H.;
 RT Coagulation factor XII (Hageman factor) Washington D.C.: inactive
 RT factor XIIa results from Cys-571->Ser substitution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322(1989).
 RP [9]
 RP VARIANT LOCARNO.
 RX MEDLINE-94325559; PubMed-8049433;
 RA Hovenga J.R., Schaller J., Stricker H., Willemin W.A., Furian M.,
 RA Laemmle B.;
 RT "Coagulation factor XII Locarno: the functional defect is caused by
 RT the amino acid substitution Arg-353->Pro leading to loss of a
 RT kallikrein cleavage site.";
 RL Blood 84:1173-1181(1994).
 RN [10]
 RP CARBOHYDRATE-LINKAGE SITE THR-109.
 RX MEDLINE-92184750; PubMed-1544894;
 RA Harris R.J., Ling V.T., Spellman M.W.;
 RT "O-linked fucose is present in the first epidermal growth factor
 RT domain of factor XII but not protein C.";
 RL J. Biol. Chem. 267:5102-5107(1992).
 CC -1- FUNCTION: FACTOR XII IS A SERUM GLYCOPROTEIN THAT PARTICIPATES IN
 CC THE INITIATION OF BLOOD COAGULATION, FIBRINOLYSIS, AND THE
 CC GENERATION OF BRADYKININ AND ANGIOTENSIN.
 CC -1- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor
 CC VII to form factor VIIa and factor XI to form factor Xla.
 CC -1- PTM: O- AND N-GLYCOSYLATED.
 CC -1- DISEASE: DEFECTS IN F12 DO NOT CAUSE ANY CLINICAL SYMPTOMS. THE
 CC SOLE EFFECT IS THAT WHOLE-BLOOD CLOTTING TIME IS PROLONGED.
 CC -1- MISCELLANEOUS: FACTOR XII, PREKALLIKREIN, AND HMW KININGEN FORM A
 CC COMPLEX BOUND TO AN ANIONIC SURFACE. PREKALLIKREIN IS CLEAVED BY
 CC FACTOR XII TO FORM KALLIKREIN, WHICH THEN CLEAVES FACTOR XI FIRST
 CC TO ALPHA-FACTOR XIa AND THEN TO BETA-FACTOR XIa. ALPHA-FACTOR
 CC XIa ACTIVATES FACTOR XI TO FACTOR Xla.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE I DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE II DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: M31315; AAA70225.1; -;
 DR EMBL: M11723; AAS1986.1; -;
 DR EMBL: M17466; AAB59490.1; -;
 DR EMBL: M17464; AAB59490.1; JOINED.
 DR EMBL: M17465; AAB59490.1; JOINED.
 DR EMBL: M13147; AAA70224.1; -;
 DR EMBL: U71274; AAB51203.1; -;
 DR PIR: A29411; KFH012.
 DR HSSP: P00750; IRTF.
 DR MEROPS: S01.211; -;
 DR MIM: 234000; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000562; FN_type_II.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Trypsin.
 DR InterPro: IPR000083; fibronectin_type_1.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00039; fn1; 1.

DR Pfam: PF00040; fn2; 1.
 DR Pfam: PF00051; kringle; 1.
 DR Pfam: PF00089; chymotrypsin.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00013; FNYPEII.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000995; FN_Type_II; 1.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00058; FN1; 1.
 DR SMART: SM00059; FN2; 1.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00022; EGF_1_2.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01253; FIBRONECTIN_1; 1.
 DR PROSITE: PS00023; FIBRONECTIN_2; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS00070; KRINGLE_2; 1.
 DR PROSITE: PS0240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein; Blood coagulation; Plasma; kringle; Serine protease;
 KW Hydrolyase; Fibrinolysis; Signal; EGF-like domain; Repeat; Zymogen;
 KW Disease mutation.
 FT SIGNAL 1 19
 FT CHAIN 20 372
 FT CHAIN 373 615
 FT CHAIN 354 362
 FT CHAIN 373 615
 FT CHAIN 47 88
 FT DOMAIN 94 131
 FT DOMAIN 133 173
 FT DOMAIN 174 210
 FT DOMAIN 217 295
 FT DOMAIN 296 349
 FT DOMAIN 373 615
 FT CARBOHYD 109 109
 FT CARBOHYD 249 249
 FT CARBOHYD 299 299
 FT CARBOHYD 305 305
 FT CARBOHYD 308 308
 FT CARBOHYD 328 328
 FT CARBOHYD 329 329
 FT CARBOHYD 337 337
 FT ACT_SITE 412 412
 FT ACT_SITE 461 461
 FT ACT_SITE 563 563
 FT DISULFID 98 110
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 135 163
 FT DISULFID 161 170
 FT DISULFID 178 189
 FT DISULFID 183 198
 FT DISULFID 200 209
 FT DISULFID 217 295
 FT DISULFID 238 277
 FT DISULFID 266 290
 FT DISULFID 359 486
 FT DISULFID 397 413
 FT DISULFID 405 475
 FT DISULFID 436 439
 FT DISULFID 500 569
 FT DISULFID 532 548

Query Match 35.5%; Score 49; DB 1; Length 615;
 Best local Similarity 41.7%; Pred. No. 15;
 Matches 10; Conservativity 5; Mismatches 7; Indels 2; Gaps 2;
 Oy 1 RNPBGVCGGWATYTNPKL-VYD 23
 Db 267 RNPBNDI-RPWCFLNDRLSWEY 289

RESULT 37
 ID PMA7_ARATH STANDARD; PRT; 961 AA.
 AC Q9LY32;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE AtPase 7, plasma membrane-type (PC 3.6.3.6) (Proton pump 7).
 GN AH47 OR AT3G60330 OR F27H5.120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustoids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RX MEDLINE=21016720; PubMed=11130713;
 RP STRAIN=CV. COLUMBIA;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unseld M.,
 RA Farmanou B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Delseny M., Boutry M., Griwell L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Choise N., Arliagave F., Robert C., Brothier P.,
 RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurnbach E., Drzonek H., Erle H., Jordan N., Bangerter S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nakamura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
 RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
 RA Cooke R., Lande M., Berger-Llauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maiese A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Aguilera A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Wees H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Uteback T., Fujii C.Y., Shea T.P.,
 RA Cressy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
 RA Pail G., Miltischer J., Sellers P., Gill J.E., Feldblum T.V.,
 RA Preuss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Frazer C.M., Kaneko T., Idesawa K., Kawashima K., Kishida Y.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa S., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana."
 RL Nature 408:820-822(2000).
 CC -1- FUNCTION: THE PLASMA MEMBRANE H+ ATPASE OF PLANTS AND FUNGI
 CC GENERATES A PROTON GRADIENT THAT DRIVES THE ACTIVE TRANSPORT OF
 CC NUTRIENTS BY H+-SYMPORT. THE RESULTING EXTERNAL ACIDIFICATION
 CC AND/OR INTERNAL ALKALINIZATION MAY MEDIATE GROWTH RESPONSES (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + H(2O) + H(+) (IN) = ADP + PHOSPHATE +
 CC H(+) (OUT).
 CC -1- SUBUNIT: BINDS TO 14-3-3 PROTEINS. THE BINDING IS INDUCED BY
 CC PHOSPHORYLATION OF THR-960. BINDING TO 14-3-3 PROTEINS ACTIVATES
 CC THE H+-ATPASE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
 CC (E1-E2 ATPASES). SUBFAMILY IIA.
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 DR EMBL: AL163852; CAB87870.1;
 DR InterPro: IPR004014; Cation_ATPase.
 DR InterPro: IPR001757; E1-E2_ATPase.

DR InterPro: IPR000695; HATPase.
 DR InterPro: IPR001454; Hydrolyase.
 DR Pfam: PF006990; Cation_ATPase_N_1.
 DR Pfam: PF00122; E1-E2_ATPase_1.
 DR Pfam: PF00702; Hydrolyase_1.
 DR PRINTS: PR00119; CATAPAPSE.
 DR PRINTS: PR00120; HATPASE.
 DR PROSITE: PS00154; ATPASE_E1_E2_1.
 KW Hydrolyase; Hydrogen ion transport; Transmembrane; Phosphorylation;
 KW ATP-binding; Metal-binding; Magnesium; Multigene family;
 KW Hypothetical protein.
 FT DOMAIN 1 64
 FT TRANSMEM 65 84
 FT DOMAIN 85 96
 FT TRANSMEM 97 117
 FT DOMAIN 118 246
 FT TRANSMEM 247 267
 FT TRANSMEM 268 276
 FT TRANSMEM 277 294
 FT TRANSMEM 295 643
 FT TRANSMEM 644 665
 FT TRANSMEM 666 670
 FT TRANSMEM 671 693
 FT TRANSMEM 694 709
 FT TRANSMEM 710 730
 FT TRANSMEM 731 764
 FT TRANSMEM 765 785
 FT TRANSMEM 786 797
 FT TRANSMEM 798 818
 FT TRANSMEM 819 826
 FT TRANSMEM 827 847
 FT TRANSMEM 848 961
 FT MOD_RES 332 332
 FT MOD_RES 960 960
 FT METAL 592 592
 FT METAL 598 598
 FT SITE 959 961
 SQ SEQUENCE 961 AA; 105520 MW; B8F965BC234A4F8 CRC64;
 Query Match 35.1%; Score 48.5; DB 1; Length 961;
 Best Local Similarity 64.3%; Pred. No. 28;
 Matches 9; Conservative 1; Mismatches 1; Indels 3; Gaps 1;
 Db 3 PDGVT---GGFWAY 13
 y145 469 PDGVTGEGGFWDF 482
 y145_METUA STANDARD; PRT; 268 AA.
 ID y145_METUA
 AC 057609;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein M0145.
 GN M0145.
 OS Methanococcus jannaschii.
 CC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 CC Methanococcus.
 CC NCBI_TaxID=2190;
 RX MEDLINE=96337999; PubMed=8688087;
 RP STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RA But C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sult G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Koverlake A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.L.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
 RA Uteback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

RA Klenk H.-P., Fraser C.M., Smith H.O., Moese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RL Science 273:1058-1073(1996).
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 CC -----
 DR EMBL: U67471; AAB98128.1; -
 DR TIGR: M0145; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 268 AA; 30285 MW; 627BBD52386B05B CRC64;
 Query Match 34.8%; Score 48; DB 1; Length 268;
 Best Local Similarity 57.1%; Pred. No. 8.7;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Oy 9 GPMATTPRKLYD 22
 Db 13 GPMVTPNPRESD 26
 RESULT 39
 PHIC_MYCTU STANDARD: PRT; 517 AA.
 AC P95245;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Phospholipase C 3 precursor (EC 3.1.4.3).
 GN PLOC OR RV2349C OR MT2414 OR MTC98.18C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Hatt D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishal W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)O = 1,2-
 CC diacylglycerol + choline phosphate.
 CC -1- MISCELLANEOUS: POLYMORPHISM WAS DISCOVERED IN THE PHOSPHOLIPASE
 CC PLCA/B/C REGION.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL PHOSPHOLIPASE C FAMILY.
 CC -----
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 CC -----
 DR EMBL: Z83860; CAB06146.1; ALT_INIT.
 DR EMBL: AE007081; AAK46707.1; ALT_INIT.
 DR TIGR: MT2414; -
 DR TubercuList; RV2349C; -
 KW Hydrolyase; Signal; Complete proteome.
 FT SIGNAL 1 24
 FT CHAIN 25 517
 SQ SEQUENCE 517 AA; 55896 MW; 5B9D4241E09755AE CRC64;
 Query Match 34.8%; Score 48; DB 1; Length 517;
 Best Local Similarity 88.9%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 NPDDGVGCP 10
 Db 205 NPDDGVGCP 213
 RESULT 40
 GAG_SIVAI STANDARD: PRT; 520 AA.
 ID GAG_SIVAI
 AC P27972;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE GAG polypeptide [contains: Core proteins P17, P24, and P15].
 GN GAG.
 OS Simian immunodeficiency virus (AGM15 isolate) (SIV-AGM).
 OS Viruses; Retrovirus; Retroviridae; Lentivirus.
 OC Viruses; Retrovirus; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90156504; PubMed=2304139;
 RA Johnson P.R., Fomsgaard A., Allan J., Gravel M., London W.T.,
 RA Olmstead R.A., Hirsch V.M.;
 RT "Simian immunodeficiency viruses from African green monkeys display
 RT unusual genetic diversity.";
 RL J. Virol. 64:1086-1092(1990).
 CC -1- MISCELLANEOUS: THE 155 ISOLATE IS FROM A MONKEY IMPORTED FROM
 CC KENYA.
 CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
 CC -----
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 CC -----
 DR EMBL: M29975; AAB91905.1; -
 DR HSSP: P03351; IED.
 DR InterPro: IPR000721; Gag_p24.
 DR InterPro: IPR000071; Retroviral_gag_p17.
 DR InterPro: IPR001878; Znf.CCHC.
 DR Pfam: PF00540; gag_p17; 1.
 DR Pfam: PF00607; gag_p24; 1.
 DR Pfam: PF00098; zf.CCHC; 2.
 DR PRINTS: PRO0939; C2HCZFNTER.
 DR PRINTS: PRO0234; HIVIMATRIX.
 DR SMART: SM00343; Znf_C2HC; 2.
 DR PROSITE: PS50158; ZF_CCHC; 2.
 KW AIDS; Core protein; Polypeptide; Zinc-finger; Repeat.
 FT CHAIN 1 141
 FT CHAIN 142 520
 FT ZN_FING 398 415
 CC CORE PROTEIN P17.
 CC CORE PROTEIN P24 AND P15.
 CC CCHC-TYPE 1.

FT ZN.FING 419 436 CCHC-TYPE 2.
 SQ SEQUENCE 520 AA; 57735 MW; 2FE1B7DBE484D414 CRC64;
 Query Match 34.1%; Score 47; DB 1; Length 520;
 Best Local Similarity 39.3%; Pred. No. 24;
 Matches 11; Conservative 2; Mismatches 5; Indels 10; Gaps 2;
 QY 1 RNPDG-DVGG-----PWATYTNPR 18
 DB 237 RDPGSDIAGTTSTVQEQLEWITYTANPR 264
 RESULT 41
 TRD5_ECOLI STANDARD; PRT; 129 AA.
 ID TRD5_ECOLI STANDARD; PRT; 129 AA.
 AC P27192;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Trad protein.
 CN TRAD.
 OS Escherichia coli.
 OG Plasmid Incp-beta R751.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RX [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-4.
 RC STRAIN-HB101;
 RX MEDLINE=92297959; PubMed=1818755;
 RA Miele L., Strack B., Kruff V., Lanka E.;
 RT "Gene organization and nucleotide sequence of the primase region of
 RT Incp plasmids RP4 and R751.";
 RL DNA Seq. 2:145-162(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Thomas C.M.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO PLASMID INCP-BETA RP4 TRAD.
 CC -----
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 CC -----
 CC EMBL; X59794; CAA42459.1; -;
 DR EMBL; U67194; AAC64471.1; -;
 DR PIR; S37670; S37670.
 KW Plasmid.
 SQ SEQUENCE 129 AA; 13600 MW; A2F7296E463BF88 CRC64;
 Query Match 33.7%; Score 46.5; DB 1; Length 129;
 Best Local Similarity 50.0%; Pred. No. 6.7;
 Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
 QY 3 PGDVGPGPWATYTNPRKLYD 22
 DB 93 PSADI-PPFITTTNARELYD 111
 RESULT 42
 ID POR2_HUMAN STANDARD; PRT; 347 AA.
 AC P45880; Q9Y516;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2)
 DE (Outer mitochondrial membrane protein porin 2).
 GN VDAC2.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-cell;
 RX MEDLINE=93280191; PubMed=7685033;
 RA Ha H., Hajek P., Bedwell D.M., Burrows P.D.;
 RT "A mitochondrial porin cDNA predicts the existence of multiple human
 RT porins.";
 RL J. Biol. Chem. 268:12143-12149(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE=93313931; PubMed=8420959;
 RA Blachly-Dyson E., Zambronicz E.B., Yu W.H., Adams V., McCabe E.R.,
 RA Adelman J., Colombini W., Forte M.;
 RT "Cloning and functional expression in yeast of two human isoforms of
 RT the outer mitochondrial membrane channel, the voltage-dependent anion
 RT channel.";
 RL J. Biol. Chem. 268:1835-1841(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RX MEDLINE=99431679; PubMed=10501981;
 RA Decker W.K., Bowles K.R., Schatte E.C., Towbin J.A., Craigen W.J.;
 RT "Revised fine mapping of the human voltage-dependent anion channel
 RT loci by radiation hybrid analysis.";
 RL Mamm. Genome 10:1041-1042(1999).
 RN [4]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=95294003; PubMed=7539795;
 RA Yu W.H., Wolfgang W., Forte M.;
 RT "Subcellular localization of human voltage-dependent anion channel
 RT isoforms.";
 RL J. Biol. Chem. 270:13998-14006(1995).
 CC -1- FUNCTION: FORMS A CHANNEL, THROUGH THE MITOCHONDRIAL OUTER
 CC MEMBRANE THAT ALLOWS DIFFUSION OF SMALL HYDROPHILIC MOLECULES.
 CC THE CHANNEL ADOPTS AN OPEN CONFORMATION AT LOW OR ZERO MEMBRANE
 CC POTENTIAL AND A CLOSED CONFORMATION AT POTENTIALS ABOVE 30-40 MV.
 CC THE OPEN STATE HAS A WEAK ANION SELECTIVITY WHEREAS THE CLOSED
 CC STATE IS CATION-SELECTIVE.
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane.
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4; are
 CC produced by alternative splicing and possibly alternative
 CC initiation.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED.
 CC -1- DOMAIN: CONSISTS MAINLY OF MEMBRANE-SPANNING SIZED BETA-SHEETS.
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC MITOCHONDRIAL PORIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; L08666; AAA60144.1; -;
 DR EMBL; L08666; AAA60145.1; -;
 DR EMBL; L06328; AAB59457.1; -;
 DR EMBL; AF152227; AAD40241.1; -;
 DR EMBL; AF152220; AAD40241.1; JOINED.
 DR EMBL; AF152221; AAD40241.1; JOINED.
 DR EMBL; AF152222; AAD40241.1; JOINED.
 DR EMBL; AF152223; AAD40241.1; JOINED.
 DR EMBL; AF152224; AAD40241.1; JOINED.
 DR EMBL; AF152225; AAD40241.1; JOINED.
 DR EMBL; AF152226; AAD40241.1; JOINED.
 DR MIM; 193245; -;
 DR InterPro: IPR001925; Euk porin.
 DR Pfam: PF01459; Euk-porin.1.
 DR PRINTS; PR00185; EUKARYTPORIN.

DR PROSITE; PS00558; EUKARYOTIC_PORIN; 1.
 KW Outer membrane; Porin; Mitochondrion; Alternative splicing;
 KW Alternative initiation; Polymorphism.
 FT VARSPLIC 1 26 MISSING (IN ISOFORM 2).
 FT VARSPLIC 1 26 M5MCNEIRLPALKOHSIGKLESHIT -> MATHGQTGAR
 P (IN ISOFORM 3).
 FT VARSPLIC 303 347 SP5WRLNPAERLWEMISEDLALIVFHCDQQAAPPED
 DONKG -> LALEEA (IN ISOFORM 4).
 FT VARIANT 39 39 A -> V.
 FT VARIANT 90 90 /FTID-VAR_006380.
 W -> C.
 SQ SEQUENCE 347 AA; 38092 MW; 23F8ACA61184A1BD CRC64;
 /FTID-VAR_006381.
 Query Match 33.3%; Score 46; DB 1; Length 347;
 Best Local Similarity 42.1%; Pred. No. 22;
 Matches 8; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

OY 7 VGSPWATTP--RKLYD 23
 DB 301 VGSPWRLNPAERLWEM 319
 RESULT 43
 GAG_SIVAT STANDARD; PRT; 519 AA.
 AC P05892;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE GAG polyprotein [contains: Core proteins P17, P24, and P15].
 GN GAG.
 OS Simian immunodeficiency virus (TYO-1 isolate) (SIV-AGM).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 NCBI_TaxID=11731;
 RN [1]
 RP MEDLINE=88232906; PubMed=3374586;
 RX MEDLINE=88232906; PubMed=3374586;
 RA Fukasawa M., Miura T., Hasegawa A., Morikawa S., Tsujimoto H.,
 RT Mikita K., Kitamura T., Hayami M.;
 RT "Sequence of simian immunodeficiency virus from African green monkey,
 RT a new member of the HIV/SIV group.";
 RT Nature 333:457-461(1988).
 CC -1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
 CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
 CC -----
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 CC -----
 DR EMBL; X07805; CAA30657.1; -;
 DR PIR; A30045; FOLJG4.
 DR HSSP; P05888; IAA.
 DR HIV; X07805; GAGSAGMTY.
 DR InterPro; IPR000721; Gag_P24.
 DR InterPro; IPR000711; Retroviral_gag_p17.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00540; gag_p17; 1.
 DR Pfam; PF00607; gag_p24; 1.
 DR Pfam; PF00098; zf-CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR PRINTS; PR00234; HIVMATRIX.
 DR SMART; SM00343; ZNF_C2HC; 2.
 DR PROSITE; PS0158; ZF_CCHC; 2.
 DR AIDS; Core protein; Polyprotein; Zinc-finger; Repeat.
 FT CHAIN 1 141 CORE PROTEIN P17.
 FT CHAIN 142 519 CORE PROTEIN P17.
 FT ZN_FING 397 414 CCHC-TYPE 1.
 FT ZN_FING 418 435 CCHC-TYPE 2.

SQ SEQUENCE 519 AA; 58143 MW; 85A3AC06BCDC38 CRC64;
 Query Match 33.3%; Score 46; DB 1; Length 519;
 Best Local Similarity 39.3%; Pred. No. 34;
 Matches 11; Conservative 2; Mismatches 5; Indels 10; Gaps 2;

OY 1 RNPDC-DVGG-----PWATTNPR 18
 DB 241 RDRGSDIAGTTSVQOLEWITYTANPR 264
 RESULT 44
 GAG_SIVAG STANDARD; PRT; 521 AA.
 AC P27978;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE GAG polyprotein [contains: Core proteins P17, P24, and P15].
 GN GAG.
 OS Simian immunodeficiency virus (AGM3 isolate) (SIV-AGM).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 NCBI_TaxID=11730;
 RN [1]
 RP MEDLINE=90232731; PubMed=2158689;
 RX MEDLINE=90232731; PubMed=2158689;
 RA Balier M., Gatter C., Mueller C., Cichutek K., Kurth R.;
 RT "Complete nucleotide sequence of a simian immunodeficiency virus from
 RT African green monkeys: a novel type of intragroup divergence.";
 RT Virology 176:216-221(1990).
 CC -1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
 CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
 CC -----
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 CC -----
 DR EMBL; M30931; AAA91913.1; -;
 DR HSSP; P03351; IEIA.
 DR InterPro; IPR000721; Gag_P24.
 DR InterPro; IPR000771; Retroviral_gag_p17.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00540; gag_p17; 1.
 DR Pfam; PF00607; gag_p24; 1.
 DR Pfam; PF00098; zf-CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR PRINTS; PR00234; HIVMATRIX.
 DR SMART; SM00343; ZNF_C2HC; 2.
 DR PROSITE; PS0158; ZF_CCHC; 2.
 DR AIDS; Core protein; Polyprotein; Zinc-finger; Repeat.
 FT CHAIN 1 145 CORE PROTEIN P17.
 FT CHAIN 146 521 CORE PROTEIN P24 AND P15.
 FT ZN_FING 402 419 CCHC-TYPE 1.
 FT ZN_FING 423 440 CCHC-TYPE 2.
 SQ SEQUENCE 521 AA; 58409 MW; 1F11B0ZF2BDF4F5 CRC64;
 Query Match 33.3%; Score 46; DB 1; Length 521;
 Best Local Similarity 39.3%; Pred. No. 34;
 Matches 11; Conservative 2; Mismatches 5; Indels 10; Gaps 2;

OY 1 RNPDC-DVGG-----PWATTNPR 18
 DB 241 RDRGSDIAGTTSVQOLEWITYTANPR 264
 RESULT 45
 FA12_CAVPO STANDARD; PRT; 603 AA.
 AC Q04962;

DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
 DE (HAF) (Fragment).
 GN F12.
 OS *Cavia porcellus* (Guinea pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
 CC NCBI_TaxID=10141;
 RP [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 19-37; 318-332 AND 359-373.
 RC T155DE-Liver;
 RX MEDLINE=93003367; PubMed=1390917;
 RA Semba U., Yamamoto T., Kunisada T., Shibuya Y., Tanase S.,
 RA Kambara T., Okabe H.;
 RA "Primary structure of guinea-pig Hageman factor: sequence around the
 RT cleavage site differs from the human molecule."
 RL Biochim. Biophys. Acta 1159:113-121(1992).
 CC -1- FUNCTION: FACTOR XII IS A SERUM GLYCOPROTEIN THAT PARTICIPATES IN
 CC THE INITIATION OF BLOOD COAGULATION, FIBRINOLYSIS, AND THE
 CC GENERATION OF BRADYKININ AND ANGIOTENSIN.
 CC -1- CATALYTIC ACTIVITY: Cleaves selectively Arg-Ile bonds in factor
 CC VII to form factor VIIa and factor XI to form factor Xla.
 CC -1- MISCELLANEOUS: FACTOR XII, PREKALLIKREIN, AND HMW KININOGEN FORM A
 CC COMPLEX BOUND TO AN ANIONIC SURFACE. PREKALLIKREIN IS CLEAVED BY
 CC FACTOR XII TO FORM KALLIKREIN, WHICH THEN CLEAVES FACTOR XII FIRST
 CC TO ALPHA-FACTOR XIIA AND THEN TO BETA-FACTOR XIIA. ALPHA-FACTOR
 CC XIIA ACTIVATES FACTOR XI TO FACTOR XIA.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE I DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE II DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: X68615; CAA48600.1; -
 CC DR HSSP: P00750; IRTF.
 DR MEROPS: S01.211; -
 DR InterPro: IPR000561; EGF_1like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR000562; FN_Type_II.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; trypsin.
 DR InterPro: IPR000083; fibronectin_type_1.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00039; fn1; 1.
 DR Pfam: PF00040; fn2; 1.
 DR Pfam: PF00051; Kringle; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRODOM: PD000995; FN_Type_II; 1.
 DR SMART: SM00181; EGF_2.
 DR SMART: SM00058; FN1; 1.
 DR SMART: SM00059; FN2; 1.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00200; TRYP_Spec; 1.
 DR PROSITE: PS00022; EGF_1; 2.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01253; FIBRONECTIN_1; 1.
 DR PROSITE: PS00023; FIBRONECTIN_2; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS00070; KRINGLE_2; 1.
 DR PROSITE: PS02040; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.

DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein: Blood coagulation; Plasma; Kringle; Serine protease;
 KW Hydrolase; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 18
 FT CHAIN 19 358
 FT CHAIN 359 603
 FT CHAIN 46 87
 FT CHAIN 93 130
 FT CHAIN 132 172
 FT CHAIN 173 209
 FT CHAIN 216 294
 FT CHAIN 312 342
 FT CHAIN 359 603
 FT CHAIN 398 398
 FT ACT_SITE 447 447
 FT ACT_SITE 551 551
 FT ACT_SITE 97 109
 FT DISULFID 103 118
 FT DISULFID 120 129
 FT DISULFID 134 162
 FT DISULFID 160 169
 FT DISULFID 177 188
 FT DISULFID 182 197
 FT DISULFID 199 208
 FT DISULFID 216 294
 FT DISULFID 237 276
 FT DISULFID 265 289
 FT DISULFID 345 422
 FT DISULFID 383 399
 FT DISULFID 391 461
 FT DISULFID 422 425
 FT DISULFID 488 557
 FT DISULFID 520 536
 FT DISULFID 547 578
 FT DISULFID 248 248
 FT CARBOHYD 270 270
 FT CARBOHYD 419 419
 SO SEQUENCE 603 AA; 66795 MW; 48DC6B946FB95ED59 CRC64;
 Query Match 33.3%; Score 46; DB 1; Length 603;
 Best Local Similarity 38.1%; Pred. No. 39;
 Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
 Db 76 PNEGDQDQWAVCLEPKVKDH 96
 3 PDGVDGGMATYTPNPKLYDY 23
 1: 1 111 1: 1: 1:
 RESULT 46
 ID YHX6_YEAST STANDARD; PRT; 373 AA.
 AC P38866;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 42.4 kDa protein in CTR2-STB5 intergenic region.
 GN YHR176W.
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC NCBI_TaxID=4932;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=S288C / AB972;
 CC MEDLINE=94378003; PubMed=8091229;
 CC Johnson M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 CC Du Z., Favellio A., Fulton L., Gattung S., Geisel C., Kirsten J.,
 CC Kucuba T., Hillier L., Jier M., Johnson L., Langston Y.,
 CC Lathreille P., Louis E.J., Macri C., Mendis S., Mouser L.,
 CC Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
 CC Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 CC Vaudin M.;

```
RT      "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome  
RT      VIIr.";  
RL      Science 265:2077-2082(1994).  
CC      -I SIMILARITY: BELONGS TO THE FMO FAMILY.  
CC      -----  
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CC      -----  
DR      EMBL; U00027; AAB68021.1; -.  
DR      PIR; S48915; S48915.  
DR      SGD; S0001219; YHR176W.  
DR      InterPro; IPR000360; FMO.  
DR      Pfam; PF00743; FMO-like; 1.  
DR      PRINTS; PR00370; FMOXYGENASE.  
DR      Hypothetical protein; Oxidoreductase; Flavoprotein; PAD.  
RW      SEQUENCE 373 AA; 42440 MW; DFB5BA11956896CB CMC64;  
  
Query Match          33.0%; Score 45.5; DB 1; Length 373;  
Best Local Similarity 39.1%; Pred. No. 28;  
Matches    9; Conservative   5; Mismatches     6; Indels    3; Gaps    1;  
  
QY       4 GDGVGGPMAY---TTNP RKLYDY 23  
           | :| | | | :| | | | |:  
Db        40 DYDIGGVMHYPEOKSGDGRVMTDH 62  
  
RESULT 47  
OASLT_HUMAN         STANDARD;             PTR:   514 AA.  
ID              OASLT_HUMAN  
AC      015646; 075686; Q9Y6K7; Q9Y6K6;  
DT      01-NOV-1997 (Rel. 35, Created)  
DT      30-MAY-2000 (Rel. 39, Last sequence update)  
DT      16-OCT-2001 (Rel. 40, Last annotation update)  
DE      59 kDa 2'-5'-oligoadenylate synthetase like protein (p59 OASLT)  
DE      (p59OASLT) (Thyroid receptor interacting protein 14) (TRIP14).  
OS      OASLT OR TRIP14.  
OS      Homo sapiens (Human).  
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX      NCBI_TaxId=9606;  
RN      [1]  
RP      SEQUENCE FROM N.A. (ISOFORM p56).  
RX      MEDLINE=98391734; PubMed=9722630;  
RA      Hartmann R., Olsen H.S., Wilder S., Joergensen R., Justesen J.;  
RT      "59OASLT, a 2'-5' oligoadenylate synthetase like protein: a novel  
RT      human gene related to the 2'-5' oligoadenylate synthetase family.";  
RL      Nucleic Acids Res. 26:4121-4127(1998).  
RN      [2]  
RP      SEQUENCE FROM N.A. (ISOFORMS p56 AND p30).  
RX      TISUE=Monoctyes;  
RC      MEDLINE=99041549; PubMed=9826176;  
RZ      Reboulillat D., Marie I., Hovanessian A.G.;  
RT      "Molecular cloning and characterization of two related and interferon-  
RT      induced 56-kDa and 30-kDa proteins highly similar to 2'-5'  
RT      oligoadenylate synthetase.";  
RL      Eur. J. Biochem. 257:319-330(1998).  
RN      [3]  
RP      SEQUENCE FROM N.A.  
RA      White S.;  
RL      Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.  
RN      [4]  
RP      SEQUENCE OF 260-416 FROM N.A. (ISOFORM p56).  
RX      MEDLINE=95295737; PubMed=7776974;  
RA      Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.;  
RT      "Two classes of proteins dependent on either the presence or absence  
RT      of thyroid hormone for interaction with the thyroid hormone  
RT      receptor.";  
RL      Mol. Endocrinol. 9:243-254(1995).
```

[illegible]

AC P43311;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Polyphenol oxidase, chloroplast precursor (EC 1.10.3.1) (PRO)
 DE (Catechol oxidase).
 OS Vitis vinifera (Grape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
 OC Vitis.
 CX NCBI_TaxID=29760;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. SULTANA; TISSUE=fruit;
 RX MEDLINE=95036022; PubMed=7948897;
 RA Dry I.B., Robinson S.P.;
 RT "Molecular cloning and characterisation of grape berry polyphenol
 RT oxidase".
 RL Plant Mol. Biol. 26:495-502(1994).
 CC -1- FUNCTION: CATALYZE THE OXIDATION OF MONO- AND O-DIPHENOLS TO O-
 CC DIQUINONES.
 CC -1- CATALYTIC ACTIVITY: 2 catechol + O(2) = 2 1,2-benzoquinone + 2
 CC H(2)O.
 CC -1- COFACTOR: BINDS TWO COPPER IONS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
 CC -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: Z27411; CA81798.1; -
 CC EMBL: A27657; CA81887.1; -
 DR InterPro: IPR002227; Tyrosinase.
 DR Pfam: PF00264; Tyrosinase; 1.
 DR PRINTS: PR00092; TYROSINASE.
 DR PROSITE: PS00497; TYROSINASE_1; 1.
 DR PROSITE: PS00498; TYROSINASE_2; 1.
 KW Oxidoreductase; Copper; Metal-binding; Chloroplast; Transit peptide.
 FT TRANSIT 1 103 CHLOROPLAST (POTENTIAL).
 FT CHAIN 104 607 POLYPHENOL OXIDASE.
 FT METAL 211 211 COPPER A (BY SIMILARITY).
 FT METAL 220 220 COPPER A (BY SIMILARITY).
 FT METAL 342 342 COPPER B (BY SIMILARITY).
 FT METAL 346 346 COPPER B (BY SIMILARITY).
 FT METAL 375 375 COPPER B (BY SIMILARITY).
 SQ SEQUENCE 607 AA; 67347 MW; B9045598B69BC57B CRC64;
 Query Match 33.0%; Score 45.5; DB 1; Length 607;
 Best Local Similarity 47.6%; Pred. No. 47;
 Matches 10; Conservative 3; Mismatches 7; Indels 1; Gaps 1;
 OY 2 NPDGVCWPMAYTTNPKLYD 22
 DB 249 NPDG-WYMPITYASSPSLYD 268
 AC 008762;
 ID NEUTR_MOUSE STANDARD; PRT; 761 AA.
 DT 30-MAY-2000 (rel. 39, Created)
 DT 30-MAY-2000 (rel. 39, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Neutrypsin precursor (EC 3.4.21.-) (Motopsin) (Brain-specific serine
 DE protease 3) (BSSP-3).
 GN PRSS12 OR BSSP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97401523; PubMed=9245503;
 RA Geschwend T.P., Kruenger S.R., Kozlov S.V., Wolfer D.P., Sonderegger P.;
 RT "Neutrypsin, a novel multidomain serine protease expressed in the
 RT nervous system".
 RL Mol. Cell. Neurosci. 9:207-219(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98008848; PubMed=9344839;
 RA Yamaguchi Y., Yamashiro K., Tsuruoka N., Nakazato H., Tsujimura A.,
 RA Yamaguchi N.;
 RT "Molecular cloning of a novel brain-specific serine protease with a
 RT kringle-like structure and three scavenger receptor cysteine-rich
 RT motifs".
 RL Biochem. Biophys. Res. Commun. 239:366-392(1997).
 CC -1- FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTEOLYTIC
 CC ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS ASSOCIATED WITH
 CC LEARNING AND MEMORY OPERATIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN CEREBRAL CORTEX, HIPPOCAMPUS
 CC AND AMYGDALA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 SRCR DOMAINS.
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 CC
 CC EMBL: Y13192; CA73646.1; -
 CC EMBL: D89871; BAA23986.1; -
 DR HSSP: P20231; IAAO.
 DR MEROPS: S01.237; -
 DR MGD: MGI:1100881; Prss12.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001190; SRCR.
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00051; Kringle; 1.
 DR Pfam: PF00530; SRCR; 3.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE; FALSE_NEG.
 DR PRINTS: PR00258; SPERACTRCPTR.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00202; SR; 3.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00021; KRINGLE_1; FALSE_NEG.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 DR PROSITE: PS00420; SRCR_1; 3.
 DR PROSITE: PS0287; SRCR_2; 3.
 DR PROSITE: PS50240; TRYPsin.DOM; 1.
 DR PROSITE: PS0134; TRYPsin.HIS; 1.
 DR PROSITE: PS00135; TRYPsin.SER; 1.
 KW Hydrolyase; Serine
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 761 NEUTROTTRYPSIN.
 FT METAL 85 157 KRINGLE.
 FT DOMAIN 166 267 SRCR 1.
 FT DOMAIN 273 373 SRCR 2.
 FT DOMAIN 386 487 SRCR 3.
 FT DOMAIN 505 761 SERINE PROTEASE.
 FT DOMAIN 505 761 ZYMOGEN ACTIVATION REGION.
 FT ACT_SITE 516 517 REACTIVE BOND (POTENTIAL).

FT ACT_SITE 562 562 CHARGE RELAY SYSTEM.
 FT ACT_SITE 612 612 CHARGE RELAY SYSTEM.
 FT ACT_SITE 711 711 CHARGE RELAY SYSTEM.
 FT DISULFID 505 636 POTENTIAL.
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 521 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 761 AA; 84118 MW; DF507B03712164E6 CRC64;

Query Match 33.0%; Score 45.5; DB 1; Length 761;
 Best Local Similarity 39.1%; Pred. No. 59;
 Matches 9; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

OY 1 RNDPDVGGPMATTPRKLYDY 23
 DB 131 RSPDGS-GRPWCERYNAOGKVDW 152

RESULT 50

FOLD_YEAST
 ID FOLD_YEAST STANDARD; PRT; 427 AA.
 AC Q12676;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Polypolylutamate synthase (EC 6.3.2.17) (Folyl)poly-gamma-glutamate
 DE synthetase (PPGS).
 GN FOL3 OR YMR13W OR YW9718.12.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
 OX NCBI_TaxId=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Hunt S., Bowman S., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=20261521; PubMed=10799479;
 RA Cherest H., Thomas D., Surdin-Kerjan Y.;
 RT "Polylutamylation of folate coenzymes is necessary for methionine
 RT biosynthesis and maintenance of intact mitochondrial genome in
 RT Saccharomyces cerevisiae."
 RL J. Biol. Chem. 275:14056-14063(2000).
 CC - FUNCTION: CONVERSION OF FOLATES TO POLYGLUTAMATE DERIVATIVES.
 CC - CATALYTIC ACTIVITY: ATP + [tetrahydrofolyl-[Glu]](N) + L-glutamate
 CC = ADP + phosphate + [tetrahydrofolyl-[Glu]](N+1).
 CC - SIMILARITY: BELONGS TO THE POLYGLUTAMATE SYNTHASE FAMILY.
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 CC -----
 DR EMBL; Z49702; CA89750.1; -;
 DR HSSP; P15925; 1FGS.
 DR SGD; S0004719; FOL3.
 DR InterPro: IPR001645; FOLYLPOLYGLU_SYN.
 DR Pfam: PF01225; Mur_Ligase; 1.
 DR PROSITE; PS01011; FOLYLPOLYGLU_SYN_1; 1.
 DR PROSITE; PS01012; FOLYLPOLYGLU_SYN_2; 1.
 KW Ligase; One-carbon metabolism; ATP-binding.
 FT NP_BIND 30 36 ATP (POTENTIAL).
 SQ SEQUENCE 427 AA; 47851 MW; C3307CEFA3BE1F30 CRC64;

Query Match 32.6%; Score 45; DB 1; Length 427;
 Best Local Similarity 37.5%; Pred. No. 38;
 Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 8 GGPMAVTTNPKLYDY 23
 DB 356 GMPWHTATDPEIKDF 371

Search completed: November 8, 2002, 09:31:41
 Job time : 12 secs

